

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 13, 2002, 17:37:34 ; Search time 16.12 Seconds
(without alignments)
1828.756 Million cell updates/sec

Title: US-09-550-103-1

Perfect score: 2031

Sequence: 1 MGNRSTADADGLAGRGPA.....YTVNAEFRRVFRKLRACC 387

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2026	99.8	387	1 DYHUD4	dopamine receptor
2	1510	74.3	367	2 I49246	D4 dopamine recept
3	683	33.6	446	1 DYRND3	dopamine receptor
4	679	33.4	400	2 G01977	d3 dopamine recept
5	675	33.2	400	2 G00013	D3 dopamine recept
6	669	32.9	446	2 I48322	dopamine receptor
7	658.5	32.4	514	2 D56849	dopamine receptor
8	645	31.8	443	1 DYHUD2	dopamine receptor
9	638	31.4	511	2 C56849	dopamine receptor
10	636.5	31.3	444	1 DYBOD2	dopamine receptor
11	631.5	31.1	444	1 DYMSD2	dopamine receptor
12	631.5	31.1	444	1 S08146	dopamine receptor
13	629.5	31.0	442	1 DYXUD2	dopamine receptor
14	581	28.6	450	2 A38316	alpha-2-adrenergic
15	574.5	28.3	450	2 A37223	alpha-2-adrenergic
16	573	28.2	484	2 S58868	G protein-coupled
17	566	27.9	450	2 A34169	alpha-2A-adrenergic
18	565.5	27.8	461	2 A31337	alpha-2C-adrenergic
19	563.5	27.7	448	2 I51883	alpha-2B-adrenergic
20	563.5	27.7	455	2 S28221	alpha-2-C2 adrener
21	560.5	27.6	453	2 A35642	serotonin receptor
22	559.5	27.5	379	2 JC6178	alpha-2B-adrenergic
23	552	27.2	458	2 A40392	alpha-2-adrenergic
24	551	27.1	450	2 I49481	alpha-2-adrenergic
25	550	27.1	450	2 B40392	alpha-2-adrenergic
26	547.5	27.0	458	2 A48392	alpha 2C adrenoce
27	547.5	27.0	458	2 I49480	alpha-2 adrenergic
28	542.5	26.7	422	2 JH0315	serotonin receptor
29	542	26.7	458	2 A37869	alpha-2B-adrenergic

30	536.5	26.4	421	2 I49375	serotonin receptor
31	532.5	26.2	476	2 JC5042	G protein-coupled
32	529	26.0	601	2 S12004	tyramine receptor
33	529	25.9	601	2 JH0170	octopamine recepto
34	527	25.9	422	2 I38209	serotonin receptor
35	527	25.9	450	2 JH0190	alpha-2-adrenergic
36	522	25.7	432	2 I50829	alpha 2-adrenocept
37	512.5	25.2	480	2 I53053	beta 1 adrenergic
38	508	25.0	400	2 S32804	beta-3-adrenergic
39	504.5	24.8	564	2 A38271	serotonin receptor
40	500.5	24.6	405	2 S65459	beta-3-adrenergic
41	500.5	24.6	418	2 G02953	beta-3-adrenergic
42	498	24.5	509	2 A47174	serotonin receptor
43	497.5	24.5	408	1 ORHUB	beta-3-adrenergic
44	497.5	24.5	414	1 ORHUB3	beta-3-adrenergic
45	495	24.4	477	1 ORHUB1	beta-1-adrenergic

ALIGNMENTS

RESULT	1	
DYHUD4		
dopamine receptor D4 - human		
C:Species: Homo sapiens (man)		
C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 02-Sep-1997		
C:Accession: S15079		
R:van Tol, H.H.M.; Bunzow, J.R.; Guan, H.C.; Sunahara, R.K.; Seeman, P.; Niznik, H.B		
Nature 350, 610-614, 1991		
A:Title: Cloning of the gene for a human dopamine D(4) receptor with high affinity f		
A:Reference number: S15079; MUID:91204054		
A:Accession: S15079		
A:Molecule type: DNA		
A:Residues: 1-387 <VAN>		
A:Cross-references: EMBL:X58497		
C:Genetics:		
A:Gene: GDB:DRD4		
A:Cross-references: GDB:127782; OMIM:126452		
A:Map position: 11p15.5-11p15.5		
A:Introns: 95/3; 133/2; 269/2; 321/1		
C:Superfamily: vertebrate rhodopsin		
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; neurotra		
F:34-60/Domain: transmembrane #status predicted <TM1>		
F:72-96/Domain: transmembrane #status predicted <TM2>		
F:110-131/Domain: transmembrane #status predicted <TM3>		
F:153-174/Domain: transmembrane #status predicted <TM4>		
F:192-214/Domain: transmembrane #status predicted <TM5>		
F:215-314/Domain: intracellular #status predicted <IN1>		
F:315-339/Domain: transmembrane #status predicted <TM6>		
F:349-368/Domain: transmembrane #status predicted <TM7>		
F:3/Binding site: carbohydrate (asn) (covalent) #status predicted		
F:108-185/Disulfide bonds: #status predicted		
F:149,239/Binding site: phosphate (Ser) (covalent) #status predicted		
F:297,306/Binding site: phosphate (Thr) (covalent) #status predicted		
Query Match: 99.8%; Score 2026; DB 1; Length 387;		
Best Local Similarity 99.7%; Pred. No. 1e-122;		
Matches 386; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
OY 1 MGNSTADADGLAGRGPAAGASAGLAGOGAAALVGVLLIGAVLAGNSLVCVSA 60		
DB 1 MGNSTADADGLAGRGPAAGASAGLAGOGAAALVGVLLIGAVLAGNSLVCVSA 60		
OY 61 TERALQPTNFSFIYSLAADLLALVLPFVYSEVGGAWILSPRLCDALMADVLC 120		
DB 61 TERALQPTNFSFIYSLAADLLALVLPFVYSEVGGAWILSPRLCDALMADVLC 120		
OY 121 ASINLCAISVDRVAVAVPLRYNRGGSSRQLLIGTWTLLSAVAVPVCGLNDVGR 180		
DB 121 ASINLCAISVDRVAVAVPLRYNRGGSSRQLLIGTWTLLSAVAVPVCGLNDVGR 180		
OY 181 DPVACRLIEDROYVYSSVCSFELPCPLMLLLYMATFRGLQWEVARRAKLHGAPRRPSG 240		

DB 181 DPVACRLDRLDQVYVSSVCSFLLPCPLMLLLYMAFRLQRMWEVARRAKLHGRARRPSG 240
|||
QY 241 PGPPSPTRPAPRLPDPCGCPDAPAPGLPPDPCGSSNAPPAVAALPQTPQTQTRR 300
|||
DB 241 PGPPSPTRPAPRLPDPCGCPDAPAPGLPPDPCGSSNAPPAVAALPQTPQTQTRR 300
|||
QY 301 RRAKTGERRKAMRLPVVGAFLLCWTPFVHTTQALCPACSVPRPLVSAVTLGYVN 360
|||
DB 301 RRAKTGERRKAMRLPVVGAFLLCWTPFVHTTQALCPACSVPRPLVSAVTLGYVN 360
|||
QY 361 SALNPVITVENAEFRNRFRKALRACC 387
|||
DB 361 SALNPVITVENAEFRNRFRKALRACC 387
|||

RESULT 2
149246
D4 dopamine receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C:Accession: 149246
R:Fishburn, C.S.; Carmon, S.; Fuchs, S.
A:Title: Molecular cloning and characterisation of the gene encoding the murine D4 dopamine
A:Reference number: 149246; MUID:95212551
A:Accession: 149246
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-387 <RES>
A:Cross-references: EMBL:U19880; NID:9758426; PIDN:AAC52190.1; PID:9758427
C:Superfamily: vertebrate rhodopsin
C:Keywords: neurotransmitter receptor

Query Match 74.3%; Score 1510; DB 2; Length 387;
Best Local Similarity 76.1%; Pred. No. 1e-89;
Matches 302; Conservative 18; Mismatches 57; Indels 20; Gaps 4;
QY 1 MGNRTAADADGLLAGRGAAGASAGSAGIAGOGAAIVGVLIGVLAGNSIVCSVA 60
|||
DB 1 MGNRTATEDGGLLAGRGP---ESTGTAGLGAGAAALGVGLLIGVLAGNSIVCSVA 57
|||
QY 61 TERALQTPNSFIVSLAADLLALLVLPFYSEVGGAMLSPLCDALMAMDVALCT 120
|||
DB 58 SERTIQTPNFVIVSLAADLLALLVLPFYSEVGGVWLSRLCDTLMAMVMTCT 117
|||
QY 121 ASIFNLCAISVDREYAVAVPLRYNRQGSRRQLLIGATWLISAAVAAPVLCGLNDVGR 180
|||
DB 118 ASIFNLCAISVDREYAVAVPLRYNRQGSRRQLLIGATWLISAAVAAPVLCGLNDVGR 175
|||
QY 181 DPVACRLDRLDQVYVSSVCSFLLPCPLMLLLYMAFRLQRMWEVARRAKLHGRARRPSG 240
|||
DB 176 DPVACRLDRLDQVYVSSVCSFLLPCPLMLLLYMAFRLQRMWEVARRAKLHGRARRPSG 235
|||
QY 241 PGPPSPTRPAPRLPDPCGCPDAPAPGLPPDPCGSSNAPPAVAALPQTPQTQTRR 290
|||
DB 236 PGPPSPTRPAPRLPDPCGCPDAPAPGLPPDPCGSSNAPPAVAALPQTPQTQTRR 290
|||
QY 291 POTPOTRRRRRAKTGERRKAMRLPVVGAFLLCWTPFVHTTQALCPACSVPRPLV 350
|||
DB 291 QPPESSRRRRRAKTGERRKAMRLPVVGAFLLCWTPFVHTTQALCPACSVPRPLV 350
|||
QY 351 SAVTWLGYVNSALNPVITVENAEFRNRFRKALRACC 387
|||
DB 351 SAVTWLGYVNSALNPVITVENAEFRNRFRKALRACC 387
|||

RESULT 3
DYKRD3
dopamine receptor D3 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999

C:Accession: S11565; S41849; I52280
R:Sokoloff, P.; Giros, B.; Martres, M.P.; Bouthenet, M.L.; Schwartz, J.C.
Nature 347, 146-151, 1990
A:Title: Molecular cloning and characterization of a novel dopamine receptor (D(3))
A:Reference number: S11565; MUID:90370111
A:Accession: S11565
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-446 <50K>
A:Cross-references: EMBL:X53944; NID:956060; PIDN:CAA37887.1; PID:956061
R:Giros, B.; Martres, M.P.; Pilon, C.; Sokoloff, P.; Schwartz, J.C.
Biochem. Biophys. Res. Commun. 176, 1584-1592, 1991
A:Title: Shorter variants of the D(3) dopamine receptor produced through various pat
A:Reference number: S41849; MUID:91248260
A:Accession: S41849
A:Molecule type: DNA
A:Residues: 1-138, 140-446 <GIR>
R:Pagliusi, S.; Cholllet-Daenierius, A.; Losberger, C.; Mills, A.; Kawashima, E.
Biochem. Biophys. Res. Commun. 194, 465-471, 1993
A:Title: Characterization of a novel exon within the D3 receptor gene giving rise to
A:Reference number: I52280; MUID:93326159
A:Accession: I52280
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 71-106 <RES>
A:Cross-references: GB:S63847; NID:9399705; PIDN:AAB27545.1; PID:9399707
A:Experimental source: strain Wistar, brain
C:Genetics:
A:Introns: 90/3
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; lipoprotein; neurotransmitter
F:33-55/Domain: transmembrane #status predicted <TM1>
F:67-92/Domain: transmembrane #status predicted <TM2>
F:105-126/Domain: transmembrane #status predicted <TM3>
F:150-172/Domain: transmembrane #status predicted <TM4>
F:186-209/Domain: transmembrane #status predicted <TM5>
F:210-375/Domain: intracellular #status predicted <CY5>
F:376-399/Domain: transmembrane #status predicted <TM6>
F:413-434/Domain: transmembrane #status predicted <TM7>
F:102-19/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:103-181/Disulfide bonds: #status predicted
F:446/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 33.6%; Score 683; DB 1; Length 446;
Best Local Similarity 37.4%; Pred. No. 8.6e-37;
Matches 154; Conservative 54; Mismatches 126; Indels 78; Gaps 8;
QY 44 LIGAVLAGNSLVCSVATERALQTPNSFIVSLAADLLALLVLPFYSEVGGAMWL 103
|||
DB 39 LILATIFGNGLVCAVLEBERALQTTNLYVSLAVALDLVTLVMPVWVYLEVGVWNE 98
|||
QY 104 SPRCLDALMAMDVALCTASIFNLCAISVDREYAVAVPLRYNR---QGSSRRQLLIGATW 160
|||
DB 99 SRICDVFVTLDDVMWCTASIINLCAISIDRYTAVVMPVHYGHGQSSCRVAMLTAVW 158
|||
QY 161 LLSAAVAVPVCGLNDVGRDPVAVCRLEDRLDQVYVSSVCSFLLPCPLMLLLYMAFRL 217
|||
DB 159 VLAFVAVSCPLPFGFNTT---GPPSISINPDVAVTSSVSVFYPGCVLVAVARYIYLR 216
|||
QY 218 GLQRMWEVARRAKLHGRARRPSGPPSPPT----- 247
|||
DB 217 QQRKRLITLRQNSQISIR-----PQPPQSSCLRLHPIRQPSIRARFLSDATGQMEHTD 272
|||
QY 248 PPAERLPDPCGCPDAPAPGL-----PPDPCGSCNAPPAVAALPQTPQTQTRR 288
|||
DB 273 KQYPQKCDPLSHLQPPSPGQTHGLKRYYSICODTLARHPSLEGAGMSPVERTNSL 332
|||
QY 289 LPQTPP---QTRRRRAKTG-----REKAMRYLPVVGAFILCWPPEF 331
|||
DB 332 SPVMAVRLKSLERKLSNGLSTSLRGLPQDQVPLRKKATQWVYVIGAFIYCWLPFF 392
|||
QY 332 VHTLQALCPACSVPRPLVSAVTLGYVNSALNPVITVENAEFRNRFRKAL 383
|||

Db 393 LTHVLNTHCQACHVSPELYRATWLGYNVSNALNPVITTFTEVFERKAKLKITL 444

RESULT

4

G01977

d3 dopamine receptor - human

C:Species: Homo sapiens (man)

C:Date: 21-Dec-1996 #sequence-revision 06-Jun-1997 #text-change 13-Aug-1999

C:Accession: G01977

R:Fishburn, C.S.; Park, B.

Submitted to the EMBL Data Library, July 1995

A:Reference number: G08971

A:Accession: G01977

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: mRNA

A:Residues: 1-400 <F1S>

A:Cross-references: EMBL:U32499; NID:927341; PIDN:AAA73929.1; PID:927342

C:Superfamily: vertebrate rhodopsin

Query Match

Best Local Similarity

Matches 155; Conservative 51; Mismatches 141; Indels 52; Gaps 8;

33.4%; Score 679; DB 2; Length 400;

Pred. No. 1.4e-36;

Query 21 GASAGASAGLAGGAGAAVGGVLLIGAVLGNLSVCSVATERALQPTNSFIYSLAAD 80

Db 16 GAENSTGASQARPHAYVALSTCALILAVFNGVLVCMALVERALQTTNTLVSLAAD 75

Query 81 LLLALLVLEFVSEVGGAMLLSPRLCDALMADVALCTASIFNLCAISYDREFAVAVP 140

Db 76 LLVATLVPMVYVLEVGNGVNFSLICDVFVTLDMVMTASILNLCAISIDRYAVVMP 135

Query 141 LRYNR---QGSRRQLLIGATWLLISAAPAVALCGLNDVGRDPACVCRLEDRIYVSS 197

Db 136 VHYHGTOGSSCRVALMITAVWVLAFAVSCPLLFGEFNT--GDPVCSISNPDEVIYS 193

Query 198 VCSFPLPCLMLLLY---WATFRGIQREWEVARAKLHGRAPRRSPGPPPTPRAPRLP 254

Db 194 VVSFLPFGVTLVARYLVKORRRKILTRQNSQNSVR-----PGFP 239

Query 255 QDPCGPD-----CAPAPAGLPP-DPCGSNCAPPAVRAALP---PQTPQTR 298

Db 240 QQTLSPPDAHLLEKRYYSICDDTALGSGFQERGELKREKTRNSLSTPTAPKLSLEVR 299

Query 299 RRRRAKITG-----RRKARVLPVVGAFLLCWPPEFVHITQALCPACS 344

Db 300 KLSNGRLSTSLKGLPGRGVPLEKREKATQVAIVLGAFIYCWLPFFLTHVLTNHCQYCH 359

Query 345 VPPRLVSAVTLGYVNSALNPVITVFNAAEERNVFRKAL 383

Db 360 VSPELYSAVTLGYVNSALNPVITTFTEVFERKAKLKITL 398

RESULT

5

G00013

D3 dopamine receptor - green monkey

C:Species: Cercopithecus aethiops (green monkey, grivet)

C:Date: 13-Mar-1997 #sequence-revision 13-Mar-1997 #text-change 13-Aug-1999

C:Accession: G00013

R:Ross, P.C.

Submitted to the EMBL Data Library, February 1995

A:Reference number: G00049

A:Accession: G00013

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: mRNA

A:Residues: 1-400 <ROS>

A:Cross-references: EMBL:U21307; NID:984965; PIDN:AAA75379.1; PID:984966

C:Superfamily: vertebrate rhodopsin

C:Keywords: neurotransmitter receptor

Query Match

33.2%; Score 675; DB 2; Length 400;

Best Local Similarity 39.9%; Pred. No. 2.5e-36;
Matches 150; Conservative 50; Mismatches 124; Indels 52; Gaps 8;

RESULT

4

G01977

d3 dopamine receptor - human

C:Species: Homo sapiens (man)

C:Date: 21-Dec-1996 #sequence-revision 06-Jun-1997 #text-change 13-Aug-1999

C:Accession: G01977

R:Fishburn, C.S.; Park, B.

Submitted to the EMBL Data Library, July 1995

A:Reference number: G08971

A:Accession: G01977

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: mRNA

A:Residues: 1-400 <F1S>

A:Cross-references: EMBL:U32499; NID:927341; PIDN:AAA73929.1; PID:927342

C:Superfamily: vertebrate rhodopsin

Query Match

Best Local Similarity

Matches 155; Conservative 51; Mismatches 141; Indels 52; Gaps 8;

33.4%; Score 679; DB 2; Length 400;

Pred. No. 1.4e-36;

Query 21 GASAGASAGLAGGAGAAVGGVLLIGAVLGNLSVCSVATERALQPTNSFIYSLAAD 80

Db 16 GAENSTGASQARPHAYVALSTCALILAVFNGVLVCMALVERALQTTNTLVSLAAD 75

Query 81 LLLALLVLEFVSEVGGAMLLSPRLCDALMADVALCTASIFNLCAISYDREFAVAVP 140

Db 76 LLVATLVPMVYVLEVGNGVNFSLICDVFVTLDMVMTASILNLCAISIDRYAVVMP 135

Query 141 LRYNR---QGSRRQLLIGATWLLISAAPAVALCGLNDVGRDPACVCRLEDRIYVSS 197

Db 136 VHYHGTOGSSCRVALMITAVWVLAFAVSCPLLFGEFNT--GDPVCSISNPDEVIYS 193

Query 198 VCSFPLPCLMLLLY---WATFRGIQREWEVARAKLHGRAPRRSPGPPPTPRAPRLP 254

Db 194 VVSFLPFGVTLVARYLVKORRRKILTRQNSQNSVR-----PGFP 239

Query 255 QDPCGPD-----CAPAPAGLPP-DPCGSNCAPPAVRAALP---PQTPQTR 298

Db 240 QQTLSPPDAHLLEKRYYSICDDTALGSGFQERGELKREKTRNSLSTPTAPKLSLEVR 299

Query 299 RRRRAKITG-----RRKARVLPVVGAFLLCWPPEFVHITQALCPACS 344

Db 300 KLSNGRLSTSLKGLPGRGVPLEKREKATQVAIVLGAFIYCWLPFFLTHVLTNHCQYCH 359

Query 345 VPPRLVSAVTLGYVNSALNPVITVFNAAEERNVFRKAL 383

Db 360 VSPELYSAVTLGYVNSALNPVITTFTEVFERKAKLKITL 398

RESULT

6

G00013

D3 dopamine receptor - green monkey

C:Species: Cercopithecus aethiops (green monkey, grivet)

C:Date: 13-Mar-1997 #sequence-revision 13-Mar-1997 #text-change 13-Aug-1999

C:Accession: G00013

R:Ross, P.C.

Submitted to the EMBL Data Library, February 1995

A:Reference number: G00049

A:Accession: G00013

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: mRNA

A:Residues: 1-446 <ROS>

A:Cross-references: EMBL:X67274; NID:950651; PIDN:CAA47691.1; PID:950652

C:Superfamily: neurotransmitter receptor

C:Keywords: neurotransmitter receptor

Query Match

32.9%; Score 669; DB 2; Length 446;

Best Local Similarity 37.2%; Pred. No. 6.8e-36;

Matches 153; Conservative 54; Mismatches 128; Indels 76; Gaps 8;

Query 44 LIGAVLGNLSVCSVATERALQPTNSFIYSLAADLLALLVLEFVSEVGGAMLL 103

Db 39 LILALIFGNGLVCAVLERALQTTNTLVVSLAADLLVATLVMPVYVLEVGWVNF 98

Query 104 SPRCLDALMADVALCTASIFNLCAISYDREFAVAVPRLYNR---QGSRRQLLIGATW 160

Db 99 SRICCDVVTLDVMCTASILNLCAISIDRYAVVMPVHYHGTOGSSCRVALMITAVW 158

Query 161 LLSAAPAVALCGLNDVGRDPACVCRLEDRIYVSSVCSFPLPCLMLLYWATFRGIQ 220

Db 159 VLAFAVSCPLLFGEFNT--GDPVCSISNPDEVIYSVSVFPGVTLVARYVWLR 216

Query 221 RMEVARRAKLGRAPR---RPSGPPPS-----PTP 248

Db 217 Q---RRRRRIILTRQNSQISIRPGPOSSCLRLHPIRQFSIRAFSLDAGOMHEIDK 273

Query 249 PAPRLPDPGCGDCAAPAPGL-----PPDPCGSCAPPAVRAAL 289

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Db      274  PYPKCQDPLSLHLQPLSPGQTHGLKRYYSICQDTALRHPREEGGQMSQVERTRNSLS 333
Qy      290  PRQPR---QTRRRRAKITG-----REKARVLVLYVYGAELLCPTPFV 332
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      334  PTMAKRLSLERKLSLNGRLSTSLKGLPLOGPCVPLREKRAKQMVIVYGAFLICWLPFEL 393
Qy      333  VHTIQLPCPACVSPRLVSAVTWGLGYNSALNPVLYTTEKNAEERVRKAL 383
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      394  THVLNTHQOACHVSPELYRATITWGLGYNSALNPVLYTTFTNIEERKFLKIL 444

RESULT 7
D56849
dopamine receptor-like protein D222 - Japanese pufferfish
C:Species: Fugu rubripes (Japanese pufferfish)
C:Date: 27-Oct-1995 #sequence_revision 27-Oct-1995 #text_change 07-May-1999
C:Accession: D56849
R:Macrae, A.D.; Brenner, S.
Genomics 25, 436-446, 1995
A:Title: Analysis of the dopamine receptor family in the compact genome of the puffer f
A:Reference number: A56849; MUID:95309911
A:Accession: D56849
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-514 <MAC>
C:Superfamily: vertebrate rhodopsin
C:Keywords: neurotransmitter receptor

```

A:Cross-references: GB:S62137; NID:g405309; PIDs:AMB26619.1; PID:g405310
C:Genetics:
A:Gene: GDB:DRD2
A:Cross-references: GDB:119852; OMIM:126450
A:Map position: 11q23.1-11q23.1
C:Introns: 178/1; 241/3; 270/3; 380/1
C:Superfamily: vertebrate rhodopsin
F:1-443/Product: alternative splicing; G protein-coupled receptor; glycoprotein; lipoprotein
F:1-443/Product: dopamine receptor D2 (long form) #status predicted <MPT1>
F:1-241-271-443/Product: dopamine receptor D2 (short form) #status predicted <MPT2>
F:38-59/Domain: transmembrane #status predicted <TM1>
F:71-94/Domain: transmembrane #status predicted <TM2>
F:109-110/Domain: transmembrane #status predicted <TM3>
F:152-114/Domain: transmembrane #status predicted <TM4>
F:188-210/Domain: transmembrane #status predicted <TM5>
F:211-373/Domain: intracellular #status predicted <CYT>
F:374-337/Domain: transmembrane #status predicted <TM6>
F:406-449/Domain: transmembrane #status predicted <TM7>
F:517-23/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:107-182/Disulfide bonds: palmitate (Cys) (covalent) #status predicted
F:443/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match	31.8%;	Score 645;	DB 1;	Length 443;
Best Local Similarity	39.1%;	Pred. NO. 2.3e-34;		
Matches 160;	Conservative 51;	Mismatches 120;	Indels 78;	Gaps 14

```

QY      43  LLIAVLAINSLVCVSAATRAALQOTPNSTIVSLAADLLILPLLEFYSVQGAU. 102
D      43  LLIIVIEGAVLYCMAVSRKALQOTTNLYLIVSLAADLLVALLVMPVWYILEV-GEUK 101
QY      103  LSPRLCALMAADVALCTASIFNLCAISVDRFVAVAVPLRYN-ROGSSRROLLEIGATWL 161
D      102  FSRHICIEFVLDVMCTASILNCAISIDRYAAMPMLXNRYSSKRRTVMIVAY 161
QY      162  LSAVAAPVYGLGDVNGRPAVCRLEDROYVYVSSVCSFELPCPLMLLYNATFGLOR 221
D      162  LSTISCPLEFLGLNNA---DQNECIANPAFVYVSSIVSEYVPEITLVLYIKIYIVLRR 218
QY      222  -----WEVRAKILGRAP-----RR-- 238
D      219  RRRKVNTRKRSSRAIRALRLAPRLKGNCTHPEDMCLITYIMKSNGSFYNNRRREVAARRAOE 278
QY      239  -----SGGPP-----SPTRPABR--LRQDPC--GPDCAAPAPGLPPDPCSGNCAPPD 282
D      279  LEMEMLSSTSPPERTRYSPISRHQTLPL-DRSHGHLSTPDSPKPE---KNGHND 333
QY      283  AVRAAL-PRQTPRQTKRRRAKTGR-----EKAAKRVLEVVYVGAELLCWTPRFVTH 334
D      334  HPKIAKIFEIOTMNGSTRISLKTMSRRKLSQOEKKATOMLAIIVGPICLCPFEITH 393
QY      335  ITOALCPACSVPRLVSAVIMGLGVNSALPVIYVYFNNEFRVAPKAL 383
D      394  ILINHCDCNIRPVLVYSAFTWMLGVNSAVNPDIYTTTNNIEERAKFTKIL 441

```

RESULT 9
C56849
dopamine receptor-like protein D215 - Japanese pufferfish
C:Species: Fugu rubripes (Japanese pufferfish)
C:Date: 27-Oct-1995 #sequence_revision 27-Oct-1995 #text_change 07-May-1999
C:Accession: C56849
R:Macrae, A.D.; Brenner, S.
Genomics 25, 436-446, 1995
A:Title: Analysis of the dopamine receptor family in the puffer fish genome
A:Reference number: A56849; MUID:95309911
A:Accession: C56849
A:Status: preliminary; not compared with conceptual translation

A;Residues: 1-511 <MAC>
C;Superfamily: vertebrate rhodopsin
C;Keywords: neurotransmitter receptor

Query Match	31.48;	Score 638;	DB 2;	Length 511;
Best Local Similarity	32.68;	Pred. No. 7.3e-34;		
Matches 155;	Conservative 62;	Mismatches 118;	Indels 140;	Gaps 10;

248	----	PAPRLP	----	ODPGPCAP	264
276	FKDSVNEBGLDELINYGSGSHKPPPPQQRALGDPATSHQLMSTKANSPISTP	3355DD			
265	PAP-----	GLPPDPCGSCNACAPDAVR	----	A	286

```

336 PPRPEGGQTEKRNKDPTEKAGGNAPAVNALNGKQTSLKTSKRKISQKEKKATQMLA 395
:287 AAP-----PPDRPPQRRRRRAKIIIGREKRAMVPIVNVGAILCMT 328
396 IYLPTRKAGGNAPAVNALNGKQTSLKTSKRKIS-QQKEKKATQMLAIVGLVFTICML 454
329 PEFVVIHTQALCPACSVPRILVSAVTWIGVYSALNPVIITYVNAEERNVFRKAL 383
455 PEFIIHTILNTHCTRCVAPKEMNAETFWIGVYSANVPDIITYTENEFFRAAFKIL 509

```

RESULT 10
DVBOD2
dopamine receptor D2 - bovine
C.Species: Bos primigenius taurus (cattle)
C.Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
C.Accession: S08163
C.Chno, C.L.: Hess, G.F.; Graham, R.S.; Huff, R.M.
Mature 343, 266-269, 1990
A.Title: A second molecular form of D2 dopamine receptor in rat and bovine caudate nucleus
A.Reference number: S08163; MUID:90136899
A.Accession: S08163
A.Status: not compared with conceptual translation

A:Residues: 1-194 <H1>
A:Cross-references: GB:X51657; NID:q304; PIDN:CAA35970.1; PID:q305
C:Superfamily: vertebrate rhodopsin
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; lipoprotein
F:1-44/Domain: transmembrane #status predicted <TM1>
F:1-211,211-444/Product: dopamine receptor D2 (long form) #status predicted <MAT1>
F:1-211,211-444/Product: dopamine receptor D2 (short form) #status predicted <MAT2>
F:39-59/Domain: transmembrane #status predicted <TM1>
F:71-94/Domain: transmembrane #status predicted <TM2>
F:109-130/Domain: transmembrane #status predicted <TM3>
F:152-174/Domain: transmembrane #status predicted <TM4>
F:188-210/Domain: transmembrane #status predicted <TM5>
F:211-374/Domain: intracellular #status predicted <CY1>
F:375-398/Domain: transmembrane #status predicted <TM6>
F:407-430/Domain: transmembrane #status predicted <TM7>
F:517-123/Binding site: carbohydrate bonds: #status predicted
F:107-182/Disulfide bonds: #status predicted
F:444/Binding site: palmitate (Cys). (covalent) #status predicted

Query Match	31.38;	Score 636.5;	DB 1;	Length 444;
Best Local Similarity	38.28;	Pred. No. 8e-34;		
Matches 155;	Conservative 53;	Mismatches 124;	Indels 75;	Gaps 13;

QY 43 LLIGAVLAGNSLVCVSVATERALQPTNSFIVSLAADDLLALVLPFVYSEVOGGAML 102
 43 LLIFIVGNLVCAVSVATERALQPTNSFIVSLAADDLLALVLPFVYSEVOGGAML 101
 QY 103 LSPRLCDALMADVALCTASTFNLCAISVDREVAAPLRYN-ROGSSRROLLIGATWL 161
 102 FSRHICDLFTVLDVMMCAISLNLCAISIDRTAVAMPMLNTRYSRRRTVMAIYVW 161
 QY 162 LSAVAAPVLCGLNDVRCRPAVCRLEDROVYVSSVCSFLLPCPLMLLWATPFGIQR 221
 162 LFTTSCPLFLGLNNT--DNECIANPAFVYSSVFSFVPTVTLVYIKIYVLRK 218
 QY 222 -----MEVARAKLHG-----RAPRRP-- 238
 219 RRRKRVNTRSSRAFRANKAPLKGNCCTHPEDMKCTVIMKSGSPVNRMRRAARRQOE 278
 QY 239 -----SGPGRP-----SPRPAPR--LPDDPC--GPDCAFPAPGLPPDPCGSCAPPD 282
 279 LEMEMLSSTSPERTRYSPIPSHQTLTP-DPSHHGLSHSPDPAKPEKNGHAKTVNPK 337
 QY 283 AVRAAALPQTPPTQTRRRRAKITGR-----ERKAMRVLPVYVGAFLCMTPEFVYHI 335
 338 IAKFEI--QSMPPNGKTFTSLKTSRRKLSQOKEKKAQOMLAIVGLVFIICWLPFFITHI 395
 QY 336 TQALCPACSVPRPLVSATVTLGYNSALNPVITVFNAEFNVRKAL 383
 396 LNIHCD-CNIPPLVLSAFTWLGYNASVNPITVTFNIEFKRAFKLIL 442

RESULT 11

DMSD2
 C:Species: Mus musculus (house mouse)
 C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
 C/Accession: S13921; JH0452; JH0453
 R:Montmayeur, J.P.; Bausero, P.; Amalaky, N.; Maroteaux, L.; Hen, R.; Borrelli, E.
 FEBS Lett. 278, 239-243, 1991
 A>Title: Differential expression of the mouse D(2) dopamine receptor isoforms.
 A:Reference number: S13921; MUID:91122293
 A:Accession: S13921
 A:Molecule type: mRNA
 A:Residues: 1-444 <MON>
 A:Cross-references: EMBL:X55674; NID:950648; PIDN:CAA39209.1; PID:950649
 J:Neurochem. 57, 795-801, 1991
 A>Title: The mouse dopamine D2A receptor gene: sequence homology with the rat and human
 A:Reference number: JH0452; MUID:91316281
 A:Accession: JH0452
 A:Molecule type: DNA
 A:Residues: 1-24, 'C', '26-28', 'P', '30-88', 'R', '90-103', 'S', '105-270', 'P', '252-444' <MANC>
 A>Note: The authors translated the codon CAG for residue 16 as Glu
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; lipoprotein;
 F:1-444/Product: dopamine receptor D2 (long form) #status predicted <MAT1>
 F:1-241,271-444/Product: dopamine receptor D2 (short form) #status predicted <MAT2>
 F:38-59/Domain: transmembrane #status predicted <TM1>
 F:71-94/Domain: transmembrane #status predicted <TM2>
 F:109-130/Domain: transmembrane #status predicted <TM3>
 F:152-174/Domain: transmembrane #status predicted <TM4>
 F:188-210/Domain: transmembrane #status predicted <TM5>
 F:211-314/Domain: intracellular #status predicted <CY1>
 F:375-398/Domain: transmembrane #status predicted <TM6>
 F:407-430/Domain: transmembrane #status predicted <TM7>
 F:5-17,23/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:107-182/Disulfide bonds: #status predicted
 F:147,148,228,229,355,360,365/Binding site: phosphate (Ser) (covalent) #status predicted
 F:225,373/Binding site: phosphate (Thr) (covalent) #status predicted
 F:444/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 31.1%; Score 631.5; DB 1; Length 444;
 Best Local Similarity 38.2%; Pred. No. 1,7e-33;

Matches 156; Conservative 51; Mismatches 126; Indels 75; Gaps 13;
 QY 43 LLIGAVLAGNSLVCVSVATERALQPTNSFIVSLAADDLLALVLPFVYSEVOGGAML 102
 43 LLIFIVGNLVCAVSVATERALQPTNSFIVSLAADDLLALVLPFVYSEVOGGAML 101
 QY 103 LSPRLCDALMADVALCTASTFNLCAISVDREVAAPLRYN-ROGSSRROLLIGATWL 161
 102 FSRHICDLFTVLDVMMCAISLNLCAISIDRTAVAMPMLNTRYSRRRTVMAIYVW 161
 QY 162 LSAVAAPVLCGLNDVRCRPAVCRLEDROVYVSSVCSFLLPCPLMLLWATPFGIQR 221
 162 LFTTSCPLFLGLNNT--DNECIANPAFVYSSVFSFVPTVTLVYIKIYVLRK 218
 QY 222 -----TFRGLOREVARAKLHG-----APRRP-- 238
 219 RRRKRVNTRSSRAFRANKAPLKGNCCTHPEDMKCTVIMKSGSPVNRMRRAARRQOE 278
 QY 239 -----SGPGRP-----SPRPAPR--LPDDPC--GPDCAFPAPGLPPDPCGSCAPPD 282
 279 LEMEMLSSTSPERTRYSPIPSHQTLTP-DPSHHGLSHSPDPAKPEKNGHAKTVNPK 337
 QY 283 AVRAAALPQTPPTQTRRRRAKITGR-----ERKAMRVLPVYVGAFLCMTPEFVYHI 335
 338 IAKFEI--QSMPPNGKTFTSLKTSRRKLSQOKEKKAQOMLAIVGLVFIICWLPFFITHI 395
 QY 336 TQALCPACSVPRPLVSATVTLGYNSALNPVITVFNAEFNVRKAL 383
 396 LNIHCD-CNIPPLVLSAFTWLGYNASVNPITVTFNIEFKRAFKLIL 442

RESULT 12

S08146
 C:Species: Rattus norvegicus (Norway rat)
 C/Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
 C/Accession: S08146; S19610; S07791; S09097; S19251; S08145; A34046; S21548;
 R:Monism J.T., F.J.; McVittie, L.D.; Gerfen, C.R.; Mahan, L.C.; Sibley, D.R.
 Nature 342, 926-929, 1989
 A>Title: Multiple D2 dopamine receptors produced by alternative RNA splicing.
 A:Reference number: S08146; MUID:90081873
 A:Accession: S08146
 A:Molecule type: mRNA
 A:Residues: 1-444 <MON>
 A:Cross-references: EMBL:X17458
 R:Chio, C.L.; Hess, G.F.; Graham, R.S.; Huff, R.M.
 Nature 343, 266-269, 1990
 A>Title: A second molecular form of D2 dopamine receptor in rat and bovine caudate nu
 A:Reference number: S08163; MUID:90136899
 A:Accession: S19610
 A:Molecule type: mRNA
 A:Residues: 1-444 <CHD>
 R:Bunzow, J.R.; Van Tol, H.H.M.; Grandy, D.K.; Albert, P.; Salon, J.; Christie, M.; t
 Nature 336, 783-787, 1988
 A>Title: Cloning and expression of a rat D(2) dopamine receptor cDNA.
 A:Reference number: S07791; MUID:89082643
 A:Accession: S07791
 A:Molecule type: mRNA
 A:Residues: 1-241,271-444 <BUN>
 A:Cross-references: EMBL:X14028
 R:Rao, D.D.; McKelvy, J.; Kebedian, J.; Mackenzie, R.G.
 FEBS Lett. 263, 18-22, 1990
 A>Title: Two forms of the rat D(2) dopamine receptor as revealed by the polymerase ch
 A:Reference number: S09040; MUID:90255966
 A:Accession: S09040
 A:Molecule type: mRNA
 A:Residues: 1-98, 'D', '100-172', 'R', '174-179', 'G', '181-444' <RAO>
 A:Cross-references: GB:X53278; NID:9288117; PIDN:CAA37373.1; PID:9288118
 R:O'Dowd, B.F.; Nguyen, T.; Tizpik, A.; Jarvie, K.R.; Israel, Y.; Seeman, P.; Niznik,
 FEBS Lett. 262, 8-12, 1990
 A>Title: Cloning of two additional catecholamine receptors from rat brain.
 A:Reference number: S09096; MUID:90201380
 A:Accession: S09097

Thu Feb 14 08:44:36 2002

us-09-550-103-1.rpr

Page 9

Search completed: February 13, 2002, 17:39:35
Job time: 121 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 13, 2002, 17:39:14 : Search time 13.31 Seconds

(without alignments)
1066.062 Million cell updates/sec

Title: US-09-550-103-1
Perfect score: 2031
Sequence: 1 MGNRSTADAGLLAGCPAA.....YTVFAEPRNVRKALRACC 387

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1976	97.3	467	1 D4DR_HUMAN	P21917 homo sapien
2	1510	74.3	387	1 D4DR_MOUSE	P51436 mus musculu
3	1496	73.7	387	1 D4DR_RAT	P10729 rattus norv
4	683	33.6	446	1 D3DR_RAT	P19020 rattus norv
5	679	33.4	400	1 D3DR_HUMAN	P25462 homo sapien
6	675	33.2	400	1 D3DR_CERAE	P2703 cervopithec
7	669	32.9	446	1 D3DR_MOUSE	P30728 mus musculu
8	657	32.3	463	1 D2DR_FUGRU	P53453 fugu rubrip
9	645	31.8	443	1 D2DR_HUMAN	P41416 homo sapien
10	644	31.7	443	1 D2DR_CERAE	P52702 cervopithec
11	636.5	31.3	444	1 D2DR_BOVIN	P20288 bos taurus
12	631.5	31.1	444	1 D2DR_MOUSE	P13953 mus musculu
13	629.5	31.0	442	1 D2DI_XENLA	P24628 xenopus lae
14	615	30.3	436	1 D2DR_MELGA	O73810 melagris g
15	581	28.6	450	1 A2AA_PIG	P18871 sus scrofa
16	575	28.3	484	1 OAR2_LOCM1	O25332 locusta mig
17	574.5	28.3	450	1 A2AB_HUMAN	P18089 homo sapien
18	574	28.3	448	1 A2AB_CAVPO	O60475 cavia porce
19	573	28.2	484	1 OAR1_LOCM1	O25331 locusta mig
20	565.5	27.8	461	1 A2AC_HUMAN	P18889 homo sapien
21	565	27.8	452	1 A2AA_BOVIN	O28888 bos taurus
22	564	27.8	455	1 A2AC_CAVPO	O60476 cavia porce
23	564	27.8	458	1 A2AD_HUMAN	P35369 homo sapien
24	563.5	27.7	455	1 A2AB_MOUSE	P30545 mus musculu
25	560.5	27.6	453	1 A2AB_RAT	P19338 rattus norv
26	559.5	27.5	379	1 GRE2_BALAM	O23127 balanus amp
27	558	27.5	450	1 A2AA_HUMAN	P08913 homo sapien
28	554	27.3	458	1 A2AC_HUMAN	P22086 rattus norv
29	552.5	27.2	450	1 A2AA_CAVPO	O60474 cavia porce
30	551	27.1	450	1 A2AA_MOUSE	O01338 mus musculu
31	547.5	27.0	450	1 A2AA_RAT	P22909 rattus norv
32	547.5	27.0	458	1 A2AC_MOUSE	O01337 mus musculu
33	542.5	26.7	422	1 SH1A_RAT	P19327 rattus norv

34	536.5	26.4	421	1 SH1A_MOUSE	O64264 mus musculu
35	532.5	26.2	476	1 GRE1_BALAM	O93126 balanus amp
36	529	26.0	601	1 OAR_DROME	P22270 drosophila
37	527	25.9	422	1 SH1A_HUMAN	P08908 homo sapien
38	522	25.7	432	1 A2AR_LABOS	O91081 labrus ossi
39	521.5	25.7	473	1 B1AR_CANFA	P79148 canis fami
40	514.5	25.3	446	1 5HT_BOMMO	O17239 bombyx mori
41	512.5	25.2	480	1 B1AR_MACMU	P47899 macaca mula
42	509.5	25.1	423	1 SH1A_FUGRU	O42385 fugu rubrip
43	508	25.0	400	1 B3AR_MOUSE	P25962 mus musculu
44	507	25.0	479	1 OAR_BOMMO	O17232 bombyx mori
45	506	24.9	405	1 B3AR_CANFA	O02662 canis fami

ALIGNMENTS

RESULT 1
ID D4DR_HUMAN STANDARD: PRT; 467 AA.
AC P21917;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE D(4) DOPAMINE RECEPTOR (D(2C) DOPAMINE RECEPTOR).
GN DRD4.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ALLELE D4.2).
RX MEDLINE=92310588; PubMed=1319557;
RA van Tol H.H., Wu C.M., Guan H.C., Ohara K., Bunzow J.R.,
RA Civelli O., Kennedy J., Seeman P., Niznik H.B., Jovanovic V.,
RT "Multiple dopamine D4 receptor variants in the human population."
RL Nature 358:149-152(1992).
RN [2]
RP SEQUENCE FROM N.A. (ALLELE D4.2).
RC TISSUE=Brain;
RX MEDLINE=91204054; PubMed=1840645;
RA van Tol H.H.M., Bunzow J.R., Guan H.-C., Sunahara R.K., Seeman P.,
RA Niznik H.B., Civelli O.;
RT "Cloning of the gene for a human dopamine D4 receptor with high
RT affinity for the antipsychotic clozapine."
RL Nature 350:610-614(1991).
RN [3]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=93038566; PubMed=1358063;
RA Livingston C.D., Strange P.G., Naylor L.H.,
RT "Molecular modelling of D2-like dopamine receptors."
RL Biochem. J. 287:277-282(1992).
RN [4]
RP VARIANT GLY-194.
RX MEDLINE=95243275; PubMed=7726213;
RA Seeman P., Ujpalan C., Chouinard G., van Tol H.H.M., Dwosch H.,
RA Lieberman J.A., Siminovich K., Liu I.S.C., Waye J., Voruganti P.,
RA Hudson C., Serleant G.R., Masibay A.S., Seeman M.V.;
RT "Dopamine D4 receptor variant, D4-glycine-194, in Africans, but not in
RT Caucasians: no association with schizophrenia.";
RL Am. J. Med. Genet. 54:384-390(1994).
CC -1- FUNCTION: THIS IS ONE OF THE FIVE TYPES (D1 TO D5) OF RECEPTORS
CC FOR DOPAMINE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G
CC PROTEINS WHICH INHIBIT ADENYLYL CYCLASE.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- POLYMORPHISM: THE NUMBER OF REPEATS IS HIGHLY POLYMORPHIC AND
CC VARIES AMONG DIFFERENT ALLELES. THE SEQUENCE SHOWN IS THAT OF
CC ALLELE D4.7.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its

DR InterPro; IPR000276; GPCR_Rhodpsn.

DR InterPro; IPR000276; GPCR_Rhodpsn.

DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSN.
 DR PRINTS: PR00242; DOPAMINER.
 DR PRINTS: PR00569; DOPAMINER.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 Multi-gene family.
 FT DOMAIN 1 34
 FT TRANSHEM 35 57
 FT DOMAIN 58 67
 FT TRANSHEM 68 90
 FT DOMAIN 91 106
 FT TRANSHEM 107 128
 FT DOMAIN 129 146
 FT TRANSHEM 147 170
 FT DOMAIN 171 186
 FT TRANSHEM 187 208
 FT DOMAIN 209 314
 FT TRANSHEM 315 337
 FT DOMAIN 338 346
 FT TRANSHEM 347 369
 FT DOMAIN 370 387
 FT CARBOHYD 3 3
 FT DISULFID 105 180
 FT CONFLICT 47 47
 FT SEQUENCE 387 AA; 41486 MW; BEA306D5E8A02E9 CRC64;
 Query Match 74.3%; Score 1510; DB 1; Length 387;
 Best Local Similarity 76.1%; Pred. No. 4.6e-78;
 Matches 302; Conservative 18; Mismatches 57; Indels 20; Gaps 4;
 DR 1 MGNSTADADGLLAGRPAAGASAGAGLAGGAGAAVGVLLIGAVLAGNSLVCSVA 60
 DB 1 MGNSSATEDGGGLLAGRGP---ESLGTGAGLGAGAGAAVGVLLIGAVLAGNSLVCSVA 57
 QY 61 TERLQPTNSFIYSLAADIALLVLPFVYSEVGGAWLSRLCDALMAMVACT 120
 DB 58 SERLQPTNSFIYSLAADIALLVLPFVYSEVGGAWLSRLCDALMAMVACT 117
 QY 121 ASINLCASIVDRFAVAVPLRYNROGSGRQLLIGATWLLSAVAAPVLCGLNDVGR 180
 DB 118 ASINLCASIVDRFAVAVPLRYNROGSGRQLLIGATWLLSAVAAPVLCGLNDVGR 175
 QY 181 DPVACLEDYVYVYSSVCSFELPCPLMLLYWATFGLQWVARAKLGRAPRRSG 240
 DB 176 DPVACLEDYVYVYSSVCSFELPCPLMLLYWATFGLQWVARAKLGRAPRRSG 235
 QY 241 PGPPSPPPARLPQDDPGPCAPAPAGLPDPGCSN-----CAPDAVAAALP 290
 DB 236 PGPPSPDP---TGGPFPPCPPLPLRLTSPSSSRPESELQSPSPGCLADALP 290
 QY 291 PGPOTRRRRRAKTTGERKAMRVLPVYGAFLLCMTPEFVHTTQALCPACSVPRLY 350
 DB 291 QPPESSRRRRRAKTTGERKAMRVLPVYGAFLLCMTPEFVHTTQALCPACSVPRLY 350
 QY 351 SAVTWLGYNSALNPVITVNAEERFNRKALRAC 387
 DB 351 SAVTWLGYNSALNPVITVNAEERFNRKALRAC 387
 RESULT 3
 DADR_RAT 3
 AC P30729; 062610; STANDARD; PRT; 387 AA.
 DT 01-APR-1993 (Rel. 25, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE D(4) DOPAMINE RECEPTOR (D(2C) DOPAMINE RECEPTOR).
 GN DRD4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 ON NCBI_TaxID=10116;
 RX SEQUENCE FROM N.A.
 RA MEDLINE=92207907; Pubmed=1554689;
 RA O'Malley K.L., Harmon S., Tang L., Todd R.D.;
 RT "The rat dopamine D4 receptor: sequence, gene structure, and
 RT demonstration of expression in the cardiovascular system.";
 RL New Biol. 4:137-146(1992).
 [2]
 RN SEQUENCE FROM N.A.
 RA Asghari V., Schouts O., Van Kats S., Ohara K., Jovanovic V.,
 RA Guan H., Bunzow J.R., Petronis A., Van Tol H.H.M.;
 RT "The dopamine D4 receptor repeat: analysis of different native and
 RT mutant forms of the human and rat gene.";
 RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: THIS IS ONE OF THE FIVE TYPES (D1 TO D5) OF RECEPTORS
 CC FOR DOPAMINE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G
 CC PROTEINS WHICH INHIBIT ADENYLYL CYCLASE.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: CENTRAL NERVOUS SYSTEM; HYPOTHALAMUS,
 CC THALAMUS; OLFACTORY BULB, AND PONTAL CORTEX.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 DR EMBL: M84009; AAA96716.1; -;
 DR EMBL: U03551; AAA18588.1; -;
 DR HSSP: P29274; 1MMH.
 DR GCRDB: GCR_0279; -;
 DR GCRDB: GCR_1032; -;
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSN.
 DR PRINTS: PR00242; DOPAMINER.
 DR PRINTS: PR00569; DOPAMINER.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 Multi-gene family.
 FT DOMAIN 1 34
 FT TRANSHEM 35 57
 FT DOMAIN 58 67
 FT TRANSHEM 68 90
 FT DOMAIN 91 106
 FT TRANSHEM 107 128
 FT DOMAIN 129 146
 FT TRANSHEM 147 170
 FT DOMAIN 171 186
 FT TRANSHEM 187 208
 FT DOMAIN 209 314
 FT TRANSHEM 315 337
 FT DOMAIN 338 346
 FT TRANSHEM 347 369
 FT DOMAIN 370 387
 FT CARBOHYD 3 3
 FT DISULFID 105 180
 FT CONFLICT 93 94
 FT SEQUENCE 387 AA; 41294 MW; 1E0A5D7452AF5050 CRC64;
 Query Match 73.7%; Score 1496; DB 1; Length 387;
 Best Local Similarity 75.1%; Pred. No. 2.8e-77;
 Matches 301; Conservative 15; Mismatches 57; Indels 28; Gaps 6;
 QY 1 MGNSTADADGLLAGRPAAGASAGAGLAGGAGAAVGVLLIGAVLAGNSLVCSVA 60
 DB 1 MGNSSATEDGGGLLAGRGP---ESLGTGAGLGAGAGAAVGVLLIGAVLAGNSLVCSVA 57

DB 1 MGNSSATGDDGGLLAGRGP---ESLGTGTGLGAGAAALVGVLLIGMVLGNSLVCVSA 57
 QY 61 TERALOTPTNSFIVSLAADLLALVLPFLFYSEVOGAMLSRLCALAMAVACT 120
 DB 58 SRRILQTPNTVIVSLAADLLALVLPFLFYSEVOGAMLSRLCALAMAVACT 117
 QY 121 ASIFNLCAISVDRFVAVAVPLRYNRGSGRRQLLITGATWLSAAVAAPVLCGLNDVGR 180
 DB 118 ASIFNLCAISVDRFVAVAVPLRYNRGSGRRQLLITGATWLSAAVAAPVLCGLNDVGR 175
 QY 181 DPACVREDRDYVYVSSVCSFLLPCPLMLLITWATFRLQRMVAVARAKLHGRAPRPSG 240
 DB 176 DPTVCELEBRDYVYVSSVCSFLLPCPLMLLITWATFRLQRMVAVARAKLHGRAPRPSG 235
 QY 241 PGCPSTPPAPRLPDGCPDCAAPAG-----LPPDPCGSCNAPPDAVA 286
 DB 236 PGCPSTPPAPRLPDGCPDCAAPAG-----LPPDPCGSCNAPPDAVA 288
 QY 287 AALPQTPOTRRRRRAKITGRERKAMRLPVVGAFLCMTPEFVHITQALCPACSV 346
 DB 289 LAQPP--APSSRRKGAKITGRERKAMRLPVVGAFLCMTPEFVHITQALCPACSV 346
 QY 347 PRLVASAVTWLGVNSALNPVITVNAERFNRKALRAC 387
 DB 347 PRLVASAVTWLGVNSALNPVITVNAERFNRKALRAC 387
 RESULT 4
 ID D3DR-RAT STANDARD: PRT: 446 AA.
 AC P19020: P70647;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE D(3) DOPAMINE RECEPTOR.
 GN DRD3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY;
 RX MEDLINE=90370111; PubMed=1975644;
 RA Sokoloff P., Giros B., Martres M.-P., Bouthenet M.-L., Schwartz J.-C.;
 RT "Molecular cloning and characterization of a novel dopamine receptor
 (D3) as a target for neuroleptics."
 RL Nature 347:146-151(1990).
 RN [2]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RX MEDLINE=91248260; PubMed=2039532;
 RA Giros B., Martres M.-P., Pilon C., Sokoloff P., Schwartz J.-C.;
 RT "Shorter variants of the D3 dopamine receptor produced through
 various patterns of alternative splicing."
 RL Biochem. Biophys. Res. Commun. 176:1584-1592(1991).
 RN [3]
 RP SEQUENCE OF 71-106 FROM N.A.
 RX MEDLINE=93326159; PubMed=8333859;
 RA Paolusini S., Chollet-Daemelin A., Losberger C., Mills A.,
 RT "Characterization of a novel exon within the D3 receptor gene giving
 rise to an mRNA isoform expressed in rat brain."
 RL Biochem. Biophys. Res. Commun. 194:465-471(1993).
 RN [4]
 RP 3D-STRUCTURE MODELING.
 RC TISSUE=Brain;
 RX MEDLINE=93038566; PubMed=1358063;
 RA Livingstone C.D., Strange P.G., Naylor L.H.;
 RT "Molecular modelling of D2-like dopamine receptors."
 RL Biochem. J. 287:277-282(1992).
 CC -1- FUNCTION: THIS IS ONE OF THE FIVE TYPES (D1 TO D5) OF RECEPTORS
 CC FOR DOPAMINE. THE ACTIVITY OF THE RECEPTOR IS MEDIATED BY G
 CC PROTEINS WHICH INHIBIT ADENYLYL CYCLASE.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: MAINLY IN LIMBIC AREAS OF BRAIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 DR EMBL: X53944: CAA37887.1; -.
 DR EMBL: M69194: AAA41076.1; ALT. SEQ.
 DR EMBL: M69189: AAA41076.1; JOINED.
 DR EMBL: M69190: AAA41076.1; JOINED.
 DR EMBL: M69191: AAA41076.1; JOINED.
 DR EMBL: M69192: AAA41076.1; JOINED.
 DR EMBL: M69193: AAA41076.1; JOINED.
 DR EMBL: A17751: CAA01349.1; -.
 DR EMBL: A17753: CAA01350.1; -.
 DR EMBL: S63847: AAB27545.1; -.
 DR EMBL: S63846: AAB27545.1; JOINED.
 DR PIR: S11565: DYR23.
 DR GCRDB: GCR_0134; -.
 DR GCRDB: GCR_0221; -.
 DR GCRDB: GCR_0236; -.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PRO0237; GPCR_Rhodopsn.
 DR PRINTS: PRO0242; DOPAMINER.
 DR PRINTS: PRO0568; DOPAMINER3.
 DR PROSITE: PS00237; G-PROTEIN_RECPT_F1_1; 1.
 DR PROSITE: PS0262; G-PROTEIN_RECPT_F2_1;
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Alternative splicing.
 FT DOMAIN 1 32
 FT TRANSMEM 33 55
 FT DOMAIN 56 66
 FT TRANSMEM 67 92
 FT DOMAIN 93 104
 FT TRANSMEM 105 126
 FT DOMAIN 127 149
 FT TRANSMEM 150 172
 FT DOMAIN 173 185
 FT TRANSMEM 186 209
 FT DOMAIN 210 375
 FT TRANSMEM 376 397
 FT DOMAIN 398 412
 FT TRANSMEM 413 434
 FT DOMAIN 435 446
 FT CARBOHYD 12 12
 FT CARBOHYD 19 19
 FT CARBOHYD 97 97
 FT CARBOHYD 173 173
 FT DISULFID 103 181
 FT VARSPPLIC 92 100
 FT VARSPPLIC 101 446
 FT VARSPPLIC 176 193
 FT CONFLICT 71 71
 FT CONFLICT 139 139
 SO SEQUENCE 446 AA; 49515 MW; 180E36AF6F217E9DB CRC64;

Query Match 33.6%; Score 683; DB 1; Length 446;
 Best Local Similarity 37.4%; Pred. No. 7.3e-32;
 Matches 154; Conservative 54; Mismatches 126; Indels 78; Gaps 8;
 QY 44 LIGAVLGNLSLVCVSVATERALQPTNSFIVSLAADLLALVLPFLFYSEVOGAMLSRLCALAMAVACT 103
 DB 39 LILATIFGNGLVCAVALERALQPTNTVNLVSLAADLLALVLPFLFYSEVOGAMLSRLCALAMAVACT 98

Query Match 33.4%; Score 679; DB 1; Length 400;
 Best Local Similarity 38.8%; Pred. No. 1,le-31;
 Matches 155; Conservative 51; Mismatches 141; Indels 52; Gaps 8;

QY 21 GASAGSAGLAGGAGAAVGLVLLIGAVLAGNSLVCSVAIERALQOTPTNSFIYSLAAD 80
 DB 16 GAENSTGASQARPHAYVALSTYCALITALVFGNGVCMVLERALQOTTNTLVYSLAAD 75
 QY 81 LLLALLVPLFVYSEVOGAMLLSPRLCDALMADVACTSIFNLCAISYDREFAVAVP 140
 DB 76 LLVATLVMPWVYVELEVINGVWNNFSRICDVFETLDVMMCTASINLCAISIDRYAVVMP 135
 QY 141 LRYNR---QGSSRQLLIGATWLLSAAVAVLGLNDVGRDPVAVCRLEDRDYVYSS 197
 DB 136 VHYHGCTGSSCRVALMTITAVWVLAFAVSCPLLFGFNTT---GDPVCSISNPDVYISS 193
 QY 198 VCSFLLPCLMLLLY---WATFRGLQREWEVARAKLHRARRRRPSPPTPAPALP 254
 DB 194 VVSFYLPGVTVLVARIYVVKORRRRLITRONSQNSVR-----PGFP 239
 QY 255 QDPCGPD-----CAPPAGLPP-DPCGSNCAPPDAVRAALP---POTPPQTR 298
 DB 240 QQTISPDPAAHLELKRYYSICODTALGPGPQERGELKREKTRNSLSPITAPKISLEVR 299
 QY 299 RRRRAKITG-----REKAMRVLPVYVGAFLCWPPEFVYVHTQALCPACS 344
 DB 300 KLSNGRLSTSLKLPLOPGVPLREKATQVAVIYLCWLPFLTHVLTNHCQYCH 359
 QY 345 VPPRLVAVTWLVYVNSALNPVITYVFAEERNNFRKAL 383
 DB 360 VSPELYSATWLVGYNSALNPVITYTTFNIEFRKAFKIL 398

RESULT 6
 D3DR CERAE STANDARD; PRT: 400 AA.
 AC P52703;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE D(3) DOPAMINE RECEPTOR.
 GN DRD3.
 OS Cercopithecus aethiops (Green monkey) (Grivet).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheciae; Cercopithecus.
 OX NCBI_Taxid=9534;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Ross P.C.;
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: THIS IS ONE OF THE FIVE TYPES (D1 TO D5) OF RECEPTORS
 FOR DOPAMINE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G
 PROTEINS WHICH INHIBIT ADENYLYL CYCLASE.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC EMBL: U21307; AAA5379.1; -
 CC GCRDB: GCR_1207; -
 CC InterPro: IPR000276; GPCR_Rhodpsn.
 CC Pfam: PF00001; 7tm.1; 1.
 CC PRINTS: PR00237; GPCRHHODPSN.
 CC PRINTS: PR00242; DOPAMINER.
 CC PRINTS: PR00568; DOPAMINED3R.

DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1;
 DR PROSITE: PS0262; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 MW MultiGene family.
 FT DOMAIN 1 32
 FT TRANSSEM 33 55
 FT DOMAIN 56 66
 FT TRANSSEM 67 92
 FT DOMAIN 93 104
 FT TRANSSEM 105 126
 FT DOMAIN 127 149
 FT TRANSSEM 150 172
 FT DOMAIN 173 185
 FT TRANSSEM 186 209
 FT DOMAIN 210 329
 FT TRANSSEM 330 351
 FT DOMAIN 352 366
 FT TRANSSEM 367 388
 FT DOMAIN 389 400
 FT CARBOHYD 12 12
 FT CARBOHYD 19 19
 FT CARBOHYD 97 97
 FT CARBOHYD 173 173
 FT DISULFID 103 181
 SQ SEQUENCE 400 AA; 44336 MW; 9358843CB0BA698B CRC64;

Query Match 33.2%; Score 675; DB 1; Length 400;
 Best Local Similarity 39.9%; Pred. No. 1,9e-31;
 Matches 150; Conservative 50; Mismatches 124; Indels 52; Gaps 8;

QY 44 LIGAVLAGNSLVCSVAIERALQOTPTNSFIYSLAADLLALLVPLFVYSEVOGAMLL 103
 DB 39 LILAIVGNGVCMVLERALQOTTNTLVYSLAADLVATLVMPWVYVELEVINGVWNNF 98
 QY 104 SPRLCDALMADVACTSIFNLCAISYDREFAVAVPLRYNR---QGSSRQLLIGATW 160
 DB 99 SRVCCDVEFTLDVMMCTASINLCAISIDRYAVVMPVHYHGCTGSSCRVALMTITAVW 158
 QY 161 LLSAAVAVPVLGLNDVGRDPVAVCRLEDRDYVYSSCFELCPCLMLLLY---WATFR 217
 DB 159 VLAFAVSCPLLFGFNTT---GDPVCSISNPDVYISSNPVITYTTFNIEFRKAFKIL 216
 QY 218 GLQWMEVARRAKLHRARRRRPSPPTPAPALPQDPCGPD-----CAPP 265
 DB 217 QRRKRRLITRONSQNSVR-----PGFPQQTISPRAHLELKRYYSICODT 262
 QY 266 APGLPP-DPCGSNCAPPDAVRAALP---POTPPQTRRRRAKITG----- 307
 DB 263 ALGSGPQERGELKREKTRNSLSPITAPKISLEVRKLSNGRLSTSLKLPLOPGVPL 322
 QY 308 RERKAMRVLPVYVGAFLCWPPEFVYVHTQALCPACSPPLVSAVWLVYVNSALNPVI 367
 DB 323 REKATQVAVIYLCWLPFLTHVLTNHCQYCHVSPPLYSATWLVGYNSALNPVI 382
 QY 368 YTVFAEERNNFRKAL 383
 DB 383 YTTFNIEFRKAFKIL 398

RESULT 7
 D3DR MOUSE STANDARD; PRT: 446 AA.
 ID D3DR_MOUSE
 AC P30728;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE D(3) DOPAMINE RECEPTOR.
 GN DRD3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;

RN [1]
 RC SEQUENCE FROM N.A.
 RA SRRIN-BALB/C;
 RL Fishburn C.S., David C., Carmon S., Belleli D., Fuchs S.;
 RN Submitted (JUL-1992) to the EMBL/GenBank/DBJ databases.
 RX [2]
 RX MEDLINE=9532026; PubMed=7598803;
 RA R.D., Skryabin B.V., Brosius J., Robakis N.R.;
 RT "Molecular cloning and characterization of the mouse dopamine D3
 RL receptor gene: an additional intron and an mRNA variant.";
 RL DNA Cell Biol. 14:485-492(1995).
 CC -1- FUNCTION: THIS IS ONE OF THE FIVE TYPES (D1 TO D5) OF RECEPTORS
 CC FOR DOPAMINE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G
 CC PROTEIN WHICH INHIBIT ADENYLYL CYCLASE.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: D3LONG (SHOWN HERE) AND D3SHORT;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 DR EMBL: X67274; CAA47691.1; -
 DR EMBL: S78580; AAB35066.2; -
 DR EMBL: S78574; AAB35066.2; JOINED.
 DR EMBL: S78638; AAB35066.2; JOINED.
 DR EMBL: S78577; AAB35066.2; JOINED.
 DR EMBL: S78578; AAB35066.2; JOINED.
 DR EMBL: S78579; AAB35066.2; JOINED.
 DR EMBL: S78639; AAB35066.2; JOINED.
 DR PIR: S25161; S25161.
 DR GCRDB: GCR.0449; -
 DR MGD: MGT.94925; Dtd3.
 DR InterPro: IPR00276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PRINTS: PR00242; DOPAMINER.
 DR PRINTS: PR00568; DOPAMINER3.
 DR PROSITE: PS00237; G-PROTEIN_RECEPTOR_1; 1.
 DR PROSITE: PS0262; G-PROTEIN_RECEPTOR_2; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Alternative splicing.
 FT DOMAIN 1 32
 FT TRANSSEM 33 55
 FT TRANSSEM 56 66
 FT TRANSSEM 67 92
 FT TRANSSEM 93 104
 FT TRANSSEM 105 126
 FT TRANSSEM 127 149
 FT TRANSSEM 150 172
 FT TRANSSEM 173 185
 FT TRANSSEM 186 209
 FT TRANSSEM 210 375
 FT TRANSSEM 376 397
 FT TRANSSEM 398 412
 FT TRANSSEM 413 434
 FT TRANSSEM 435 446
 FT CARBOHYD 12 12
 FT CARBOHYD 19 19
 FT CARBOHYD 97 97
 FT CARBOHYD 173 173
 FT DISULFID 103 181
 FT VARSPIC 268 288
 SQ SEQUENCE 446 AA; 49669 MW; B391C2D493B58242 CRC64;

Query Match 32.9%; Score 669; DB 1; Length 446;
 Best Local Similarity 37.2%; Pred. No. 4,4e-31;
 Matches 153; Conservative 54; Mismatches 128; Indels 76; Gaps 8;
 44 LIGAVIAGNSIYCVSVATERALQPTNSFIYSLAAADLLALVLPFYSEVGGAWL 103
 39 LIIAIIIFGNCVAVRERLQTTTVLVSLAVALLVATVMPVYILEVGGWNF 98
 104 SPRLCDALMADVALCTASIFNLCAISVDREVAVAAPLRYR---OGSRRQLLGATW 160
 99 SRTCCDFVTLIDVMCTASILNLCASIDRTAVMYVHHOGGOSCRVALMIAVW 158
 161 LLSAAVAPVLCGLNDYGRDPAYCRLDRDYVYSSVCSFELPCMLLLMATEFGQL 220
 159 VLAVASOPLLEFGNTT--GPSICISINPDVYSSVSVSPGVTVLVARIYVLR 216
 221 RWEVARAKLHGRAPR---RSGPGPPS-----PTP 248
 217 Q---RRRRRLTRNSOCISIRPGFPQSSCLRLHPTRFISIRAFSLDATGMEHIEDK 273
 249 PAPRLPDGPGDCAFPAPGL-----PPDGSNCAPPDAVRAAL 289
 274 PYPKCDPLLSHQPLSPGTHGELKRYISICODTALRHPNFGGMSOVERTNLS 333
 290 PPGTP---QTRRRRAKITG-----REKARVLPVVGAFLLCMTPEFV 332
 334 PTMAPKLSLEVRKLSNGLSLKLGPLQPGVPLREKKAQMVYIVGAFVCMPLPFL 393
 333 VHTQALCPACSVPPRLVSAVTWLGYNALNPVYIVFNEFRNFRKAL 383
 394 THVLNTHQACHVSPPELYRATTWLGYNALNPVYITTFNIEFRKAL 444
 RESULT 8
 ID D2DR_FUGRU STANDARD; PRT; 463 AA.
 AC P53453;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, last sequence update)
 DT 01-OCT-1996 (Rel. 34, last annotation update)
 DE D(2)-LIKE DOPAMINE RECEPTOR.
 GN Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Acanthomorpha; Acanthopterygii; Perciformes; Tetraodontiformes;
 OC Tetraodontidae; Takifugu.
 OX NCBI_TaxID=31033;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95309911; PubMed=7789977;
 RA Machae A.D., Brenner S.;
 RT "Analysis of the dopamine receptor family in the compact genome of
 RL the puffer fish Fugu rubripes.";
 RL Genomics 25:436-446(1995).
 CC -1- FUNCTION: RECEPTOR FOR DOPAMINE.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 DR EMBL: X80175; CAA56456.1; -
 DR GCRDB: GCR.1107; -
 DR InterPro: IPR00276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PRINTS: PR00242; DOPAMINER.
 DR PROSITE: PS00237; G-PROTEIN_RECEPTOR_1; 1.

DR PROSITE: PS0262; G-PROTEIN_RECEP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 Multi-gene family.
 FT DOMAIN 1 35
 FT TRANSSEM 36 58
 FT DOMAIN 59 69
 FT TRANSSEM 70 95
 FT DOMAIN 96 106
 FT TRANSSEM 107 128
 FT DOMAIN 129 149
 FT TRANSSEM 150 172
 FT DOMAIN 173 187
 FT TRANSSEM 188 211
 FT DOMAIN 212 392
 FT TRANSSEM 393 416
 FT DOMAIN 417 425
 FT TRANSSEM 426 449
 FT DOMAIN 450 463
 FT CARBOHYD 10 10
 FT CARBOHYD 16 16
 FT CARBOHYD 22 22
 FT DISULFID 105 183
 SO SEQUENCE 463 AA; 52120 MW; A54B178D7718AF6B CRC64;
 Query Match Best Local Similarity 32.3%; Score 657; DB 1; Length 463;
 Matches 151; Conservative 64; Mismatches 121; Indels 90; Gaps 8;
 QY 43 LLIGAVLAGNSLVCVSVATERALQPTNSFYSLAADLLALVLPFYSEVGGAML 102
 DB 41 LLIFVYGVNVLVCMAVSREKALQTTNYLLVSLAVADLVATLVMPVYVLEVV-GEWR 99
 QY 103 LSPRLCDLAMDVALCTASIFNLCAISVDRFAVAAPLRYNRGGSGRRRL-LLIGATWL 161
 DB 100 FSKIHCDIFVLIDVDMCTASLNLCAISIDRTAVAMMLINTKSSRRVYTMISYVWV 159
 QY 162 LSAVAAPVLCGLNDVGRDPAVCRLEDRDYYVYSSVCFELPGLMLLVYATFEGIOR 221
 DB 160 LSFALSCPLFLGLNLTARQDSLCF IANPAFVYSSVSYFVPLVTLVYVQIYVLRK 219
 QY 222 WEVARRALHGRAPRR--PSGPGPSPPTPAAPRLPDOP----- 257
 DB 220 ---RRKRVNTRKPKRQLQADPDPLSLDKCHPEDEVRRLCTMIKNSGSPVKKKVI 275
 QY 258 -----CGPDCAFPAPGLPDPCCGNCAPPD---AVAAALP---P 291
 DB 276 FIKQGVNVEGLEDELNLYCGSHKQPPQOQPALGDTPATSHOILNMTANASPTSTP 335
 QY 292 QTPQTRRR-----RRAKITGREKAMRYLP 317
 DB 336 PTPPEEGRTKNGDPTEKAGCNAPAVVALNCKTQTSLSKTLKRKIQOQEKATQMLA 395
 QY 318 VVVGAFLLCMTPEFVNVHTQALCPACSVPRVLSAVTLGLVNSALNVIYTFVNAEFRN 377
 DB 396 IVLGVFIICWLPFTIHTLHCTCKCKVPAEMYNATWLGYSANVNPITYTFNVEBRK 455
 QY 378 VERRAL 383
 DB 456 AFIKIL 461
 RESULT 9
 ID D2DR_HUMAN STANDARD; PRT; 443 AA.
 AC P14416;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE D(2) DOPAMINE RECEPTOR.
 GN DRD2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90126238; PubMed=2533064;
 RA Seibie L.A., Hayes G., Shine J.;
 RT "The major dopamine D2 receptor: molecular analysis of the human D2A
 subtype.";
 RL DNA 8:683-689(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90076122; PubMed=2531656;
 RA Dal-Toso R., Sommer B., Ewert M., Herb A., Pritchett D.B., Bach A.,
 RA Shivers B.D., Seeburg P.H.;
 RT "The dopamine D2 receptor: two molecular forms generated by
 alternative splicing.";
 RL EMO J. 8:4025-4034(1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=90206805; PubMed=2138729;
 RA Robakis N.K., Mohammadi M., Fu D.Y., Sambamurti K., Refolo L.M.;
 RT "Human retina D2 receptor cDNAs have multiple polyadenylation sites
 and differ from a pituitary clone at the 5' non-coding region.";
 RL Nucleic Acids Res. 18:1299-1299(1990).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9009344; PubMed=2532362;
 RA Grandy D.K., Marchionni M.A., Makam H., Stofko R.E., Alfano M.,
 RA Frothingham L., Fischer J.B., Burke-Howle K.J., Bunzow J.R.,
 RA Server A.C., Civelli O.;
 RT "Cloning of the cDNA and gene for a human D2 dopamine receptor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:9762-9766(1989).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Retina;
 RX MEDLINE=90136534; PubMed=2137193;
 RA Stormann T.M., Gula D.C., Weiner D.M., Brann M.R.;
 RT "Molecular cloning and expression of a dopamine D2 receptor from
 human retina.";
 RL Mol. Pharmacol. 37:1-6(1990).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9100955; PubMed=2144985;
 RA Seibie L.A., Hayes G., Shine J.;
 RT "DNA homology screening: isolation and characterization of the human
 D2 dopamine receptor subtype.";
 RL Adv. Second Messenger Phosphoprotein Res. 24:9-14(1990).
 RN [7]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93264902; PubMed=1363862;
 RA Ataki K., Kuwano R., Morik K., Hayashi S., Minoshima S.,
 RA Shimitzu N., Katagiri T., Usui H., Kumashiro T., Takahashi Y.;
 RT "Structure and expression of human and rat D2 dopamine receptor
 genes.";
 RL Neurochem. Int. 21:91-98(1992).
 RN [8]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92076439; PubMed=1835903;
 RA Deary A., Falardeau P., Shores C., Caron M.G.;
 RT "D2 dopamine receptors in the human retina: cloning of cDNA and
 localization of mRNA.";
 RL Cell. Mol. Neurobiol. 11:437-453(1991).
 RN [9]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=93228763; PubMed=8471125;
 RA Seeman P., Ohara K., Uhlman C., Seeman M.V., Jellinger K.,
 RA Tol H.H., Niznik H.B.;
 RT "Schizophrenia: normal sequence in the dopamine D2 receptor region
 that couples to G-proteins. DNA polymorphisms in D2.";
 RL Neuropsychopharmacology 8:137-142(1993).
 RN [10]

FT	SITE	194	194	(BY SIMILARITY).
FT				IMPLICATED IN RECEPTOR ACTIVATION
FT				(BY SIMILARITY).
FT	SITE	197	197	IMPLICATED IN RECEPTOR ACTIVATION
FT				(BY SIMILARITY).
FT	CARBOHYD	5	5	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	17	17	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	23	23	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	107	182	BY SIMILARITY.
FT	VARSPLIT	242	270	MISSING (IN SHORT ISOFORM).
FT	VARIANT	311	311	S -> C (IN SCHIZOPHRENICS).
FT				/FTSD-VAR_003462.
FT	CONFLICT	40	40	L -> R (IN REF.?).
SO	SEQUENCE	443 AA;	50619 MW;	9BF8EA36C98BAZE2 CRC64;
<hr/>				
Query Match				
Best Local Similarity 31.8%; Score 645; DB 1; Length 443;				
Matches 160; Conservative 51; Mismatches 120; Indels 78; Gaps 14;				
OY	43	LLIAGVLAGNSLVCVSATERALQTPNLSFVLSSLAADLLALLPLFLVSEVOGGAML	102	
PB	43	LLIAVIYEGNVLYCMASREKALQTITNYLLSLAVADLLAATLVMPVVYLEV-GEKK	101	
OY	103	LSPRCLDALMADVALCTASFIFNICASVDPRVAAYDLRYN-ROGSRROLLIGATWL	161	
PB	102	FSTRHCDFEVLDDVMCMSTAILNLCAISIDRYTAMAMELTNTRRSKRRTVMISIVW	161	
OY	162	LSAAVAPVLCGLMDVRDRPAVCRLEDRODVVVSVSCSFLPCMLMLTWATRGQR	221	
PB	162	LSFTISCLEGLGNNA---DONECIANPARVYSSIVSFVPFIYTLVLIYIKITIYLR	218	
OY	222	-----WEVARAKLIHGAP-----	238	
PB	219	RKRKVNRKRSSRAIRAHRLAPLKGCNCPHEDMKLCTVIMKNSGRPVARRVEARRQE	278	
OY	239	-----SGGP-----SPTRPADP--LPDDPC--GPDCAAPABGLPPDCGSNCAPPD	282	
PB	279	LEMELMSTSPERTRYSPIDPSHQTLTP-DPSHHGLSHSPDSAPKE---KNGHAKD	333	
OY	283	AVRAAL-PQTPPTQTRRRRAKITGR-----ERKMRLPVVYGAFLLCMTPEFPVH	334	
PB	334	HPKIAKFETQTPMGKRTSLKTWSRKLSQOKERRKATOMAIYLGVFIIICWPFITTH	393	
OY	335	ITQALCPACSVPRPLVASVTMLGVYNALSANVINIYVFAAEFRNRRKKL	383	
PB	394	ILNHCD-CNIPVLYSAFTWLGVNASVNPIITTYTFIERKKAPLKIL	441	
<hr/>				
RESULT	10			
D2DR CERAE	ID	D2DR CERAE	STANDARD:	PRT: 443 AA.
AC	P52702;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	D(2) DOPAMINE RECEPTOR.			
GN	DRD2.			
OS	Cercopithecus aethiops (Green monkey) (Grivet).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;			
OC	Cercopithecoidea; Cercopithecus.			
OX	NCBI_Taxid=9534;			
RP	[1]			
RC	SEQUENCE FROM N.A.			
RA	TISSUE=Brain;			
RA	MEDLINE=95302446; PubMed=7783157;			
RA	Thurkauf A., Hutchinson A., Peterson J., Cornfield L., Meade R.,			
RT	Houston K., Harris K., Ross P.C., Garber K., Ramabhadran T.V.,			
RT	2-phenyl-4-(aminomethyl)imidazoles as potential antipsychotic			
RT	agents. Synthesis and dopamine D2 receptor binding."			
TL	J. Med. Chem.38:2251-2255(1995).			
UC	- FUNCTION: THIS IS ONE OF THE FIVE TYPES (D1 TO D5) OF RECEPTORS			

CC FOR DOPAMINE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G
 CC PROTEINS WHICH INHIBIT ADENYLAT. CYCLASE.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U18547; AAB60369.1; -
 DR GCRDb: GCR_1209; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHHODPSN.
 DR PRINTS: PR00242; DOPAMINER.
 DR PRINTS: PR00567; DOPAMINER2.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_FL1; 1.
 DR PROSITE: PS00262; G-PROTEIN_RECEP_FL2; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein;
 KM Multiene family.
 FT DOMAIN 1 37
 FT TRANSSEM 38 60
 FT DOMAIN 61 71
 FT TRANSSEM 72 97
 FT DOMAIN 98 106
 FT TRANSSEM 109 130
 FT DOMAIN 131 151
 FT TRANSSEM 152 174
 FT DOMAIN 175 186
 FT TRANSSEM 187 210
 FT DOMAIN 211 373
 FT TRANSSEM 374 397
 FT DOMAIN 398 405
 FT TRANSSEM 406 429
 FT DOMAIN 430 443
 FT SITE 193 193
 FT SITE 194 194
 FT SITE 197 197
 FT SITE 197 197
 FT CARBOHYD 5 5
 FT CARBOHYD 17 17
 FT CARBOHYD 23 23
 FT DISULFID 107 182
 SQ SEQUENCE 443 AA; 50590 MW; 34165BE6460B524D CRC64;
 Query Match 31.7%; Score 644; DB 1; Length 443;
 Best Local Similarity 39.08; Pred. No. 1,le-29;
 Matches 159; Conservative 52; Mismatches 121; Indels 76; Gaps 14;

DB 279 LEMEMISTSPERTRYSDIPSHHQLTP-DPSHHGLHSPDSPA-KPEKNHAKNHPK 336
 QY 283 AVRAALPPQPPQTRRRRAKTIGR-----EKARVLPVVGALLLWTFPEVYHI 335
 DB 337 IAKIFEI--QTPMGKRTSLKTSRRRLSOQEKKAVALYGVFIILWLPFTTHI 394
 QY 336 TQALCPACSPVPLVSAVWTLGYNSALNPVITYFNAEFNFRKAL 383
 DB 395 LNIHCD-CNIPVLSAFTWLGYNASVNPILITTFNIEFKAKFLIL 441
 RESULT 11
 D2DR BOVIN STANDARD; PRT; 444 AA.
 ID D2DR BOVIN
 AC P20288;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE D(2) DOPAMINE RECEPTOR.
 GN DRD2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OC Bovidae; Bovinae; Bos.
 ON NCBI_Taxid=9913;
 RX MEDLINE=90136899; Pubmed=2137198;
 RA Chio C.L., Hess G.F., Graham R.S., Huff R.M.;
 RT "A second molecular form of D2 dopamine receptor in rat and bovine
 RT caudate nucleus.";
 RL Nature 343:266-269(1990).
 CC -1- FUNCTION: THIS IS ONE OF THE FIVE TYPES (D1 TO D5) OF RECEPTORS
 CC FOR DOPAMINE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G
 CC PROTEINS WHICH INHIBIT ADENYLAT. CYCLASE.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A
 CC SHORT FORM. ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X51657; CAA35970.1; -
 DR PIR: S08163; DYBOD2.
 DR GCRDb: GCR_0488; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHHODPSN.
 DR PRINTS: PR00242; DOPAMINER.
 DR PRINTS: PR00567; DOPAMINER2.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_FL1; 1.
 DR PROSITE: PS00262; G-PROTEIN_RECEP_FL2; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein;
 KM Multiene family; Alternative splicing.
 FT DOMAIN 1 37
 FT TRANSSEM 38 60
 FT DOMAIN 61 71
 FT TRANSSEM 72 97
 FT DOMAIN 98 108
 FT TRANSSEM 109 130
 FT DOMAIN 131 151
 FT TRANSSEM 152 174
 FT DOMAIN 175 186
 FT TRANSSEM 187 210
 FT DOMAIN 211 374
 FT TRANSSEM 375 398
 FT TRANSSEM 375 398

Query Match	Best Local Similarity	31.3%	Score 636.5	DB 1	Length 444
Matches 156	Conservative 53	Mismatches 124	Indels 75	Gaps 13	
QY 43	LLIGAVLAGNSLVCSVATERRALQTPNTSFIVSLAAADLLALLVPLFVSEVGGAWL	102			
DB 43	LLIFVIFGVNVLCAVMSREKALQTPNTYLLIVSLAVADLLVATVMPVYILEV -GEWK	101			
QY 103	LSPLICDALMDVALLCTRASTFNLCALISYDFRVAAVPLRYN -ROGGSRRDILLIGATWL	161			
DB 102	FSRICHDFEVTLDVMCKTASILNLCALISIDRTAAVAMPMLYNTRYSSKRRVTVMIAVW	161			
QY 162	LSAAVAAPVLGCVNVRGDPVACVREDDDVYVSSVCSFPLPCMLLLMYATFGLOR	221			
DB 162	LSFTISCPMLFGLNLT---DNECETIANFAFVYSSIVSFVPLVTLVLYIKIYIVLRR	218			
QY 222	-----WEVARAKLHG-----	238			
DB 219	RKRVTNTRKSSAFRANLKLAPLKGKCTHREDMKLCTVIMKNSGFPVNRVREAAARAE	278			
QY 239	-----SGCPDP-----SPTPPAPR---LPDQPC--GPDCAAPADGLPPDCCGSCNCPAD	282			
DB 279	LEMENLSTSPERTRYSPISPHNQLPLP-DPSHHGLSTPDSAPKPEKNHAKTVNPK	337			
QY 283	AVRAAALPQPPQPPQRRRRRAKITGR-----EKAMVLRVVVVCAGFLCMTTPFVVNI	335			
DB 338	IAKIEFI--QSPNGKTRFSLKTMGRKLSQCKEKAQIOMLIVGLVFTICMLPFEITHI	395			
QY 336	TQALCPACSVPRSLVSAVTWTLGYVNSALNPVITYVFENAEFRVAFKAL	383			
DB 396	LNHHDD-CNIPRPVLYLSAFTWLGCVNSAVNPITYTTFNIEFRFAFLKIL	442			
RESULT 12					
D2DR_MOUSE					
ID D2DR_MOUSE	STANDARD:	PRT:	444 AA.		
NC P13953:					
DT 01-JAN-1990	(Rel. 13, Created)				
DT 01-JAN-1990	(Rel. 13, Last sequence update)				
DT 20-AUG-2001	(Rel. 40, Last annotation update)				
DE D(2)	DOPAMINE RECEPTOR.				
GN DRD2.					
OS Mus musculus (Mouse), and					
OS Rattus norvegicus (Rat).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Mammalia; Euteria; Rodentia; Sciurognathi; Sciurognathi; Murinae; Mus.					
NC NCB1_Taxid=10090, 10116;					
RN [1]					
RP SEQUENCE OF 1-241 AND 271-444 FROM N.A.					
RC SPECIES-Rat; TISSUE-Brain;					
RX MEDLINE=89082643; PubMed=2974511;					
RA Bunzow J.R., van Tol H.H.M., Grandy D.K., Albert P., Salon J.,					
RT Christie M., Machida C.A., Neve K.A., Civelli O.,					
RL "Cloning and expression of a rat D2 dopamine receptor cDNA.";					
RN Nature 336:783-787(1988).					
[2]					

RP SEQUENCE FROM N.A.
RC SPECIES-Rat;
RX MEDLINE=90081866; PubMed=2531846;
RA Elime K.A., Taylor P.L., Zavaavik J., Saunders P.T.K., Inglis J.D.;
RT "D2 receptor, a missing exon."
RL Nature 342:865-865(1989).
[3]
RP SEQUENCE FROM N.A.
RC SPECIES-Rat;
RX MEDLINE=90081872; PubMed=2531847;
RA Gltos B., Sokoloff P., Martres M.-P., Riou J.-F., Emorine L.J.,
RA Schwartz J.-C.;
RT "Alternative splicing directs the expression of two D2 dopamine
RT receptor isoforms."
RL Nature 342:923-926(1989).
[4]
RP SEQUENCE FROM N.A.
RC SPECIES-Rat;
RX MEDLINE=90081873; PubMed=2480527;
RA Monsma F.J., Jr., McVittie L.D., Gerfen C.R., Mahan L.C., Sibley D.R.;
RT "Multiple D2 dopamine receptors produced by alternative RNA
RT splicing."
RL Nature 342:926-929(1989).
[5]
RP SEQUENCE FROM N.A.
RC SPECIES-Rat;
RX MEDLINE=90235966; PubMed=2139615;
RA Rao D.D., McKelvy J., Kebabian J., Mackenzie R.G.;
RT "Two forms of the rat D2 dopamine receptor as revealed by the
RT polymerase chain reaction."
RL FEBS Lett. 263:18-22(1990).
[6]
RP SEQUENCE FROM N.A.
RC SPECIES-Rat; STRAIN=SPRAGUE-DAWLEY;
RA Taylor P.L., Inglis J.D., Elime K.A.;
RL Submitted (OCT-1990) to the EMBL/Genbank/DBD databases.
[7]
RP SEQUENCE OF 242-270 FROM N.A.
RC SPECIES-Rat;
RX MEDLINE=90147685; PubMed=2137336;
RA Miller J.C., Mang Y., Flier D.;
RT "Identification by sequence analysis of a second rat brain cDNA
RT encoding the dopamine (D2) receptor."
RL Biochem. Biophys. Res. Commun. 166:109-112(1990).
[8]
RP SEQUENCE OF 242-270 FROM N.A.
RC SPECIES-Rat;
RX MEDLINE=90201380; PubMed=2138567;
RA O'Dowd B.F., Nguyen T., Tlirpak A., Jarvie K.R., Israel Y., Seeman P.,
RA Niznik H.B.;
RT "Cloning of two additional catecholamine receptors from rat brain."
RL FEBS Lett. 262:8-12(1990).
[9]
RP SEQUENCE FROM N.A. (ISOFORM A).
RC SPECIES-Mouse;
RX MEDLINE=91122293; PubMed=1991517;
RA Montmayeur J.P., Bausero P., Amalaky N., Maroteaux L., Hen R.,
RA Borrelli E.;
RT "Differential expression of the mouse D2 dopamine receptor isoforms."
RL FEBS Lett. 278:239-243(1991).
[10]
RP MUTAGENESIS OF SER-193; SER-194; SER-197 AND SER-420.
RC SPECIES-Rat;
RX MEDLINE=92333328; PubMed=1321233;
RA Cox B.A., Henningsen R.A., Spanoyannis A., Neve R.L., Neve K.A.;
RT "Contributions of conserved serine residues to the interactions of
RT 119dms with dopamine D2 receptors."
RL J. Neurochem. 59:627-635(1992).
[11]
RP INTERACTION WITH NEURABIN II.
RC MEDLINE=99321921; PubMed=10391935;
RA Smith F.D., Oxford G.S., Milgram S.L.;
RT "Association of the D2 dopamine receptor third cytoplasmic loop with

RT	sphnophilin, a protein phosphatase-1-interacting protein..";
RJ	J. Biol. Chem. 274:19894-19900(1999).
RP	[12]
RQ	3D-STRUCTURE MODELING.
RR	MEDLINE=93038566; PubMed=1358063;
RS	Livingsone C.D., Strange P.G., Naylor L.H.;
SA	"Molecular modelling of D2-like dopamine receptors.";
RA	Biochem. J. 287:277-282(1992).
RL	-I- FUNCTION: THIS IS ONE OF THE FIVE TYPES (D1 TO D5) OF RECEPTORS FOR DOPAMINE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEIN WHICH INHIBIT ADENYLYL CYCLASE.
CC	-I- SUBUNIT: INTERACTS WITH NEURABIN II.
CC	-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC	-I- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC	-I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC	-----
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CC	-----
DR	EMBL; X53278; CA337373.1; -
DR	EMBL; M32241; AAAA1074.1; -
DR	EMBL; M36831; AAAA1075.1; -
DR	EMBL; X56065; CA339543.1; -
DR	EMBL; X55674; CA339209.1; -
DR	PIR; S08146; S08146.
DR	PIR; S13921; DYMSD2.
DR	PIR; S21348; S21548.
DR	GCRDB; GCR_0095; -
DR	GCRDB; GCR_0133; -
DR	GCRDB; GCR_0135; -
DR	GCRDB; GCR_0415; -
DR	GCRDB; GCR_1468; -
DR	MGI; MGI:94924; DTG2.
DR	InterPro; IPR000276; GPCR_Rhodpsn.
DR	Pfam; PF00037; 7tm_1; 1.
DR	PRINTS; PR00237; GPCRHODPSN.
DR	PRINTS; PR00242; DOPAMINER.
DR	PRINTS; PR00567; DOPAMINER2.
DR	PROSITE; PS00237; G_PROTEIN_RECPT_FL_1; 1.
DR	PROSITE; PS50262; G_PROTEIN_RECPT_FL_2; 1.
KW	Multi-tyrosine family; Alternative splicing.
FT	DOMAIN 1 37
FT	TRANSMEM 38 60
FT	DOMAIN 61 71
FT	TRANSMEM 72 97
FT	DOMAIN 98 108
FT	TRANSMEM 109 130
FT	DOMAIN 131 151
FT	TRANSMEM 152 174
FT	DOMAIN 175 186
FT	TRANSMEM 187 210
FT	DOMAIN 211 374
FT	TRANSMEM 375 398
FT	DOMAIN 399 406
FT	TRANSMEM 407 430
FT	DOMAIN 431 444
FT	DOMAIN 211 374
FT	SITE 193 193
FT	SITE 194 194
FT	SITE 197 197
FT	CARBOHYD 5
FT	CARBOHYD 17
FT	CARBOHYD 23
FT	DISULFID 107 182
FT	VARSPLIT 242 270
FT	MOTAGCN 193 193
FT	MISSING (TN SHORT ISOFORM).
FT	S-2A: MODERATE DECREASE IN LIGAND

[illegible]

QY	239	SGPGP-----SPTPARRLPDPCPD---CAPPA-----PGLEPPDCGS	276
Db	267	AGKHPEDEMEMEMSTSPPEKTKHKRSASPDHNOIAVPATSNQCKNASLTSPESESYKAEK	326
QY	277	NCAPDAVR-AAALPPCPPPTERRRRRAKING-----REKKAMRYLPPVVGAFLLCWT	328
Db	327	NGHRKDSKPAKVEIQSMNGKTRTSTKTKSSKKLSQHKREKKATOMLAIVLGVFIITWL	386
QY	329	PEFVHTIQTALCPACSVPPRLVSAVTWLGYNVSNALNPVITYTVFNAEFPNRVERKAL	383
Db	387	PEFIHLILNMHC-NCNIPQALYSAFMTWLGYNVSNALNPVITYTVFNAEFPNRVERKAL	440
		RESULT 14	
ID	D2DR_MELGA	STANDARD:	PRT: 436 AA.
AC	073810:		
DT	20-AUG-2001	(Rel. 40, Created)	
DT	20-AUG-2001	(Rel. 40, Last sequence update)	
DT	20-AUG-2001	(Rel. 40, Last annotation update)	
DE	D(2)	DOPAMINE RECEPTOR.	
GN	DRD2.		
OS	Meleagris gallopavo	(Common turkey).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Archosauaria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.		
OX	NCBI_TaxID=9103;		
RP	[1]		
RC	SEQUENCE FROM N.A.		
RC	SPRAIN-NICHOLAS LARGE WHITE; TISSUE=Brain;		
RA	Schmell S.A., You S., Foster D.N., el Halawani M.E.;		
RT	"Molecular cloning and tissue distribution of an avian D2 dopamine		
RT	receptor from the domestic turkey (Meleagris gallopavo).";		
RL	Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.		
CC	-1- FUNCTION: THIS IS ONE OF THE FIVE TYPES (D1 TO D5) OF RECEPTORS		
CC	FOR DOPAMINE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G		
CC	PROTEINS WHICH INHIBIT ADENYLYL CYCLASE (BY SIMILARITY).		
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.		
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.		
CC	-----		
CC	This SWISS-Prot entry is copyright. It is produced through a collaboration		
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CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; AF056201; AAD03818.1; "		
DR	InterPro; IPR000276; GPCR_Rhodpsn.		
DR	Pfam; PF00001; 2tm.1; 1.		
DR	PRINTS; PR00237; GPCRHHODPSN.		
DR	PRINTS; PR00242; DOPAMINER.		
DR	PRINTS; PR00567; DOPAMINED2R.		
DR	PROSITE; PS00237; G-PROTEIN_RECPEP_F1_1; FALSE_NEG.		
DR	PROSITE; PS00262; G-PROTEIN_RECPEP_F1_2; 1.		
KW	G-protein coupled receptor; Transmembrane; Glycoprotein;		
KW	Multigene family.		
FT	DOMAIN 1	34	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	35	1 (POTENTIAL).
FT	DOMAIN	58	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	69	2 (POTENTIAL).
FT	DOMAIN	95	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	106	3 (POTENTIAL).
FT	DOMAIN	128	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	148	4 (POTENTIAL).
FT	DOMAIN	149	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	172	5 (POTENTIAL).
FT	DOMAIN	184	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	208	6 (POTENTIAL).
FT	DOMAIN	367	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	391	7 (POTENTIAL).
FT	DOMAIN	399	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	422	
FT	DOMAIN	423	

1

07 183 AVCRIEDD---YVYSSVCSEFLPCPLMLLYNATFRGLQREVAR----- 227

Db 184 ABRCEINDQKVVYISSCISGFAPCLIMILV-----VRIYQIAKRTRVPPSRGPD 237
QY 228 --AKLHGRAPRRRSGCGPP-----SPTPPAPRLPQDPCGPDCAIPA 266
Db 238 AAAALPGAEARRRPGGLPERGVGVAEAPLPVQUNGAGGEPAPAGPRDADGIDLEESS 297
QY 267 PG---LPPDPCGSNCAPDPAVRAA-----LP-----POTPPOTRRRRRA 303
Db 298 SSEHAERPPGPRRSEKPRAKSKARASQVAPGDSLPRRGAGAGGAPATGAGEERGVA 357
QY 304 KIT-----GRERKAMRVLPVVGAFLLCMTPEFVHITOALCPACSVPPRLVASAVTWLG 357
Db 358 KASRMGRQNRREKFTFVLAVIGVFVCMPPFFFTYTLAV--GCSVPPTLFKFFFWFG 415
QY 358 YVNSALNPVIYTVFNAEERNVKRAL 383
Db 416 YCNSSLNPVIYTIFFNHDFRRAFKIL 441

Search completed: February 13, 2002, 17:42:34
Job time: 200 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 13, 2002, 17:38:59 ; Search time 25.44 Seconds

(without alignments)
225.133 Million cell updates/sec

Title: US-09-550-103-1

Perfect score: 2031
Sequence: 1 MGNRSTADADGLLAGRGPAA.....YTVFNAEFNRVFKALRACC 387

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL_17:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mhcc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1034	50.9	374	13	042322 cyprinus ca
2	774	38.1	278	13	042321 cyprinus ca
3	658.5	32.4	309	4	Q13167 homo sapien
4	658.5	32.4	514	13	Q9PSA6 fugu rubrip
5	645	31.8	443	4	Q9PSA6 fugu rubrip
6	644	31.7	445	4	Q9PSA6 fugu rubrip
7	638	31.4	511	13	Q9PSA7 fugu rubrip
8	637.5	31.4	414	6	Q9GK99 canis fami
9	635.5	31.3	414	6	Q9GK99 canis fami
10	624	30.7	443	6	Q9GK99 canis fami
11	623.5	30.7	374	13	042320 cyprinus ca
12	577	28.4	447	4	Q9BZK0 homo sapien
13	574.5	28.3	399	5	Q9NG02 apis mellif
14	567	27.9	419	5	Q9NG02 apis mellif
15	566	27.9	462	4	Q9HB49 homo sapien
16	557	27.4	450	4	Q9BZK1 homo sapien
17	527	25.9	419	4	Q9P205 gorilla gor
18	527	25.9	419	6	Q9N2E1 gorilla gor
19	527	25.9	422	6	Q9N297 gorilla gor

20	526	25.9	419	6	Q9N2E2	Q9N2E2 pan troglod
21	526	25.9	419	6	Q9N2E0	Q9N2E0 pongo pygma
22	526	25.9	422	6	Q9N298	Q9N298 pan troglod
23	526	25.9	422	6	Q9N296	Q9N296 pongo pygma
24	521	25.7	408	13	Q9N898	Q9N898 xenopus lae
25	516	25.4	394	5	Q9NHR3	Q9NHR3 alysia cal
26	515.5	25.4	407	6	Q9MZ00	Q9MZ00 sus scrofa
27	503	24.8	394	5	Q9N2S6	Q9N2S6 alysia cal
28	495.5	24.4	477	5	Q9BMA9	Q9BMA9 mamesera br
29	489	24.1	603	5	Q9VG57	Q9VG57 drosophila
30	487	24.0	402	5	Q4198	Q4198 apis mellif
31	486.5	24.0	405	6	Q9GJ56	Q9GJ56 apis mellif
32	485.5	23.9	405	6	Q9GL57	Q9GL57 ovis aries
33	485.5	23.9	405	6	Q9GJ56	Q9GJ56 ovis aries
34	484.5	23.9	405	6	Q9GL56	Q9GL56 ovis aries
35	484	23.8	383	6	Q9GL28	Q9GL28 bradyus tr
36	484	23.8	508	5	Q9VC23	Q9VC23 drosophila
37	483	23.8	389	6	Q9GL07	Q9GL07 phoca vitul
38	482.5	23.8	559	11	Q9QW71	Q9QW71 rattus sp.
39	482.5	23.8	571	6	Q9TW9	Q9TW9 sus scrofa
40	481	23.7	391	6	Q9GL06	Q9GL06 sus scrofa
41	480	23.6	383	6	Q9GL20	Q9GL20 cynopterus
42	476.5	23.5	385	5	Q24038	Q24038 drosophila
43	474	23.3	885	5	Q61232	Q61232 lymanaea sta
44	473	23.3	393	6	Q9GL16	Q9GL16 hippopotamu
45	473	23.3	393	6	Q9GL15	Q9GL15 macrotus ca

ALIGNMENTS

RESULT 1

042322 PRELIMINARY; PRT; 374 AA.
ID 042322;
AC 042322;
DT 01-JAN-1998 (TREMBLREL. 05, Created)
DT 01-JAN-1998 (TREMBLREL. 05, Last sequence update)
DT 01-JUN-2001 (TREMBLREL. 17, Last annotation update)
DE DAB DOPAMINE RECEPTOR.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
OX NCBI_Taxid=7962;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=RETINA;
RA Hirano J., Archer S.N., Djangoz M.B.A.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: Y14633; CAA74977.1;
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR InterPro: IPR002106; AA_tRNA_ligase_II.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00339; AA_tRNA_LIGASE_II_2; UNKNOWN_1.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
SQ SEQUENCE 374 AA; 42004 MW; 8DE52E86B8BA717 CRC64;

Query Match 50.9%; Score 1034; DB 13; Length 374;
Best Local Similarity 54.6%; Pred. No. 1.8e-65;
Matches 214; Conservative 43; Mismatches 89; Indels 46; Gaps 6;

QY	22	ASAGSAGLAGAAGAAATGGVLLIGAVLAGNSLVCVSATERRATQPTNSFVSLAADL 81
DB	3	ANLASSHSSTNVNPPALIFGLIIIIICGVNIVCLSVYTERKALKTTNTYIVSLAVDL 62
QY	82	LLALLVLPFLVYSEVQGAWLLSPRLCDALAMADVACTASIFNICAISVDRFAVAAPL 141
DB	63	LLAVLVLPFLVYAEFQDQVMSLNTLCGLMTDMVCLTASIFNICAISIDRFVAVSIFL 122
QY	142	RYNNGGSRRLDILIGATWLLSAVAAPVLCGLNDVGRDRAVCRLEDRDVIYSSVCSF 201

[illegible]

283 AVRAAL-PQTPOTRRRRRAKIGR-----ERKAMRVLPVVGAFLLCMTPEFVH 334
Db HPKIAKEIOTMNGKRTSLKTRSRKLSQOKERKATOMAIYLGVIICMLPFETH 393
QY 335 ITQALCPACSVPRPLVSAVTMLGYNSALNPIYTVFNAEFRRVFKAL 383
Db 394 ILINHCD-CNIPPLYSAFTWLGYNASVNPITYTFTEFRKAPKIL 441
RESULT 6
Q9NZR3 PRELIMINARY; PRT; 445 AA.
AC Q9NZR3;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE DOPAMINE RECEPTOR D2LONGER.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN STRIATUM;
RX MEDLINE=20185651; PubMed=10719223;
RA Seeman P., Nam D., Ulfman C., Liu I.S.C., Tallierico T.;
RT "New dopamine receptor, D2(longer), with unique 7c splice site, in
human brain.";
RL Brain Res. 76:132-141(2000).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF176812; AAF61479.1;
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCRHOPOPSN.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 445 AA; 50846 MW; 11674E96E087F66 CRC64;
Query Match 31.7%; Score 644; DB 4; Length 445;
Best Local Similarity 38.9%; Pred. No. 6.5e-38;
Matches 160; Conservative 51; Mismatches 120; Indels 80; Gaps 14;
QY 43 LITGVLVAGNSLVCVSVTERALOPTNSFVLSLAADLLALVLPLEFVSEVGGAWL 102
Db 43 LITAVIVGNVLCMAVSREKALQTTNYLVLSLAVDLVATLVMPVNVLEVY-GERK 101
QY 103 LSPRLDALMADVALCTASIFNLCAISVDRFVAVAPLRYN-ROGSGSRQLLIGATWL 161
Db 102 FSRHCDIFVTLVDVWMCASILNLCALISIDRTAVAMPMLNTRKSSRRTVMISYIW 161
QY 162 LSAVAANVLCGLNDYRDRPAVCRLEDRDYVYSSVCSFLLPCPLMLLTYWAFRGLQR 221
Db 162 LSFITSCPLLEGLNNA---DNECELIANPAFVYSSIVSFYVPIVTLVYIKITYLVR 218
QY 222 -WEVARAKLHGRAP-----RRP 238
Db 219 RRRKVNTRSSRAFAHLRALPKGCTHPEDMKLCTVIMKNSGSPVNRNRVVOEAHRA 278
QY 239 -SGGPP-----SPTPRAPR--LPDPC--GPCCAPAPGLPPDPCGNCAP 280
Db 279 QELEMEMLSSTSPERTYSPILPSHQTLRP-DSHHGLMSTPDSAPKPE-----KNHA 333
QY 281 PDVAARAAL-PPQTPOTRRRRRAKIGR-----ERKAMRVLPVVGAFLLCMTPEFV 332
Db 334 KDHPRIAKIFEIOTMNGKRTSLKTRSRKLSQOKERKATOMAIYLGVIICMLPFI 393
QY 333 VHIQALCPACSVPRPLVSAVTMLGYNSALNPIYTVFNAEFRRVFKAL 383
Db 394 THILINHCD-CNIPPLYSAFTWLGYNASVNPITYTFTEFRKAPKIL 443

RESULT 7
Q9PSA7 PRELIMINARY; PRT; 511 AA.
AC Q9PSA7;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE D2-TYPE DOPAMINE RECEPTOR HOMOLOG.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95309911; PubMed=7789977;
RA Macrae A.D., Brenner S.;
RT "Analysis of the dopamine receptor family in the compact genome of the
puffer fish Fugu rubripes.";
RL Genomics 25:436-446(1995).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCRHOPOPSN.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
SQ SEQUENCE 511 AA; 57333 MW; 615DAC74D8C9A08E CRC64;
Query Match 31.4%; Score 638; DB 13; Length 511;
Best Local Similarity 32.6%; Pred. No. 2e-37;
Matches 155; Conservative 62; Mismatches 118; Indels 140; Gaps 10;
QY 43 LITGVLVAGNSLVCVSVTERALOPTNSFVLSLAADLLALVLPLEFVSEVGGAWL 102
Db 41 LITVIVGNVLCMAVSREKALQTTNYLVLSLAVDLVATLVMPVNVLEVY-GERK 99
QY 103 LSPRLDALMADVALCTASIFNLCAISVDRFVAVAPLRYNROGSGSRQL-LLIGATWL 161
Db 100 FSKIHCDIFVTLVDVWMCASILNLCALISIDRTAVAMPMLNTRYSRRTVMISYIW 159
QY 162 LSAVAANVLCGLNDYRDRPAVCRLEDRDYVYSSVCSFLLPCPLMLLTYWAFRGLQR 221
Db 160 LSFATISCPLEGLNNTATRDGSLCFIANPAFVYSSIVSFYVPIVTLVYQIYVLRK 219
QY 222 WEVARAKLHGRAPR-PSGGPPSP-----ODPCGPCAP 264
Db 220 -RRKVNTRKPRORLCAQADPDIPSTLKKKCHPEYRCLTMIVNSGSPVNRKKVI 275
QY 248 -----PPAPRLP-----ODPCGPCAP 264
Db 276 FIKDGVNEGLELDELNYCGSGSHKOPPOQOPALGDPATSHQLMSTRKANSPTSP 335
QY 265 PAP-----GLPPDPCGNCAPPDVAV-----A 286
Db 336 PTPPEGORTKENDPDKRAOGNPAVVALNKGRTQTSLSKTRKKSQOKERKATOMLA 395
QY 287 AALP-----PQTPOTRRRRRAKIGRERKAMRVLPVVGAFLLCMT 328
Db 396 IYLPTRKAGNPAVVALNRKNTQTSLSKTRKKSIS-QOKERKATOMAIYLGVIICWL 454
QY 329 PEFVHIQALCPACSVPRPLVSAVTMLGYNSALNPIYTVFNAEFRRVFKAL 383
Db 455 PEFTHILNHTCTCKYDAEMYNFTWLGYNASVNPITYTFTEFRKAPKIL 509
RESULT 8
Q9GK99 PRELIMINARY; PRT; 414 AA.
ID Q9GK99

Query Match	31.4%;	Score 637.5;	DB 6;	Length 414;
Best Local Similarity	37.8%;	Pred. No. 1.7e-37;		
Matches 148;	Conservative 58;	Mismatches 113;	Indels 73;	Gaps 9

RESULT	9		
Q9GKA0			
ID	Q9GKA0	PRELIMINARY;	PRT; 414 AA.
AC	Q9GKA0;		
DT	01-MAR-2001	(TREMBLrel. 16, Created)	
DT	01-MAR-2001	(TREMBLrel. 16, Last sequence update)	
DT	01-JUN-2001	(TREMBLrel. 17, Last annotation update)	
DE	DOPEAMINE D2 RECEPTOR SHORT ISOFORM.		
CS	DRD2.		
CS	Canis familiaris (Dog)		

Query Match	31.3%	Score 635.5;	DB 6;	Length 414;
Best Local Similarity	41.0%;	Pred. No. 2.4e-37;		
Matches 157;	Conservative 48;	Mismatches 123;	Indels 55;	Gaps 12

RESULT	10	
096JUI		
ID	096JUI	PRELIMINARY; PRT; 443 AA.
AC	096JUI;	
DT	01-MAR-2001 (TREMBLrel. 16, Created)	
DT	01-MAR-2001 (TREMBLrel. 16, last sequence update)	
DT	01-JUN-2001 (TREMBLrel. 17, last annotation update)	
DE	DOPAMINE D2 RECEPTOR.	
GN	DRD2.	
OS	Canis familiaris (Dog).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.	
OX	NCBI_TaxID=9615;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
FX	MEDLINE=20510028; PubMed=11054572;	
HA	Myeong H., Jeoung D., Kim H., Ha J.H., Lee Y., Kim K.H., Park C.,	

RESULT	11		
042320			
ID	042320	PRELIMINARY;	PRT; 374 AA.
AC	042320;		
DT	01-JAN-1998 (TREMBLrel. 05, Created)		
DT	01-JAN-1998 (TREMBLrel. 05, last sequence update)		
DT	01-JUN-2001 (TREMBLrel. 17, last annotation update)		
DE	D2 DOPAMINE RECEPTOR (FRAGMENT).		
OS	Cyprinus carpio (Common carp).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;		
OC	Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.		
OX	NCBI_Taxid=7962;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=RETINA;		
RA	Hirano J., Archer S.N., Djamgoz M.B.A.;		
RL	Submitted (AUG-1997) to the EMBL/Genbank/DBJ databases.		
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)		
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.		
DR	EMBL: Y14632; CAAI4976.1; -		
DR	InterPro: IPR000276; GPCR_Rhodpsn.		
DR	Pfam: PF00001; 7tm_1; 1.		

RESULT	12	
09BZKO	ID	09BZKO
	PRELIMINARY:	PRT: 447 AA.
AC	09BZKO:	
DT	01-JUN-2001 (TREMBLrel. 17, Created)	
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)	
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)	
DE	ALPHA 2B ADRENERGIC RECEPTOR.	
GN	ADRA2B.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	Pubmed=11056163;	
RA	Small K.M., Brown K.M., Forbes S.L., Liggett S.B.;	
RT	"Polymorphic Deletion of Three Intracellular Acidic Residues of the	
RT	alpha 2B-Adrenergic Receptor Decreases G Protein-coupled Receptor	
RT	kinase-mediated Phosphorylation and Desensitization.";	
RL	J. Biol. Chem. 276:4917-4922(2001).	
DR	EMBL: AFJ16895; AAK01633.1; -.	
KW	Receptor.	
FT	VARIANT	298
FT	SEQUENCE	447 AA: 49566 MW: B33D4B5B719C1C45 CRC64;
FT	EEB -> KRR.	300
FT	Match	28.4%: Score 577; DB 4; Length 447;
FT	Best Local Similarity	33.6%: Fred. NO. 3.4e-33;
FT	Matches 148; Conservative	66; Mismatches 125; Indels 102; Gaps


```

Db 10 QATPAIAAATFLILFTIFGNALVTLAVLSRSLRAPQNLFLVSLAADILVATLILPFS 69
QY 92 YVSVVGGANLSPRLCDALMADVALCTASIFNLCAISVDREVAVAVPLRYNRQGGSR 151
Db 70 LANELL-GYVYFRRTWCEVYVADVLCTSSIVHLCAISIDRYVAWSRALEYNKSRTPRR 128
QY 152 QLLIGATWTLISAANAAPVLCGLND---VRGRPAVCRL-EDRDYVYVSVCSFELPCP 206
Db 129 IKCILTTLWTLIAAVISPLPLIKGDGQPRGRPO--CKLNQEWYTLASSIGSFAPCL 186
QY 207 LMLLLYATWATERGLQRMWEVARAKLHGRAPRRSGPPSPPTPAP-----RLP--- 254
Db 187 LMLIVY-----LRIYLIAKRS--NRGAPRAKGGPGGESQPRPDHGAALASKLPALA 238
QY 255 -----ODPCGPCAPPAPELPPDP-----CGSN----- 277
Db 239 SVASAREVNGHSKSTGEKGETPEDTGTALPSPMALPNSGQCGKEGVCASPEDEAE 298
QY 278 -----CAP---PDAVRAAALPPOTPPOTRR-----RRRA 303
Db 299 EEEEEECEQOAVPSPASCPPLQOPGSRVLATLRQGVLLGRVGATGGQMMRRRA 358
QY 304 KITGERKKARVLPVVVGAFLCWTPEFVVHITQALCPA-CSVPPRLVSAVTWLVYNSA 362
Db 359 QLT-REKRFTEFLAVVIGVFLCMFPFFFSISGALCPKHKCKVPHGLQFFFTWIGYCNSS 417
QY 363 LNPVITYVENAEFRNRVKAL 383
Db 418 LNPVITYIFNQDFERRRRLIL 438

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RESULT 13

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09NG02 ID 09NG02 PRELIMINARY; PRT; 399 AA.
AC 09NG02;
DT 01-OCT-2000 (Tremblrel..15, Created)
DT 01-OCT-2000 (Tremblrel..15, Last sequence update)
DT 01-JUN-2001 (Tremblrel..17, Last annotation update)
DE G-PROTEIN COUPLED RECEPTOR.
GN TYRL.
OS Apis mellifera (Honeybee).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Apidae; Apis.
OX NCBI_TaxID=7460;
RN [1]
RP SEQUENCE FROM N.A.
RA Bienen W., Balfanz S., Baumann A.;
RT "Amyrl: characterization of a gene from honeybee (Apis mellifera)
RT brain encoding a functional tyramine receptor.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AJ245824; CAB76374.1;
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm.1.1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G-PROTEIN_RECP_F1_1.
DR PROSITE: PS50262; G-PROTEIN_RECP_F1_2.1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ
SEQUENCE 399 AA; 44650 MW; F5FE4E4F13336433 CRC64;

```

```

Query Match 28.3%; Score 574.5; DB 5; Length 399;
Best Local Similarity 37.6%; Pred. No. 4; 6e-33;
Matches 150; Conservative 66; Mismatches 158; Indels 25; Gaps 13;

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QY 2 GNSTADADGLAGRGPAAGASAGSLAGGAAALVGVLLIGAVLAGSLVCVAVT 61
Db 8 GGVWTEYD--WTCGCPPE-EFTGSNLPVWEAASLTLGLVATVATL-GAALVLSVFT 63
QY 62 ERALQPTNSFIVSLAADDLLALVLPFVYSEVGGANLSPRLCDALMADVALCTA 121

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Db 64 YRPLRIQNEFTIVSLAADLAVALLVWP-FVAVLLLLGKWTFFGLHCKMLTVCVLCCTA 122
QY 122 SIENLCAISVDREVAVAVPLRYNRQGGSRRLILIGATWTLISAANAAPVLCGLND-VRGR 180
Db 123 SILNLCAIALDRYVAIDPILNYAOKRFLKVLATVAGWILSGAISSPLAGNDWPEEL 182
QY 181 DPAV-CLEDD-IVVYVSVCSFELPCMLL---LYMAFRLQRMWEVARAKKLG-- 232
Db 183 EPGPCQLTRQGVYVYISLGSFIPILLMSLVLEYLAVLRRLR--ERRAQRINAVQ 240
QY 233 RAPPRLPGCPSPPTP-----PAPRLDPCGPCAPPAPEPPPCGSCNCAPPAVR 285
Db 241 STRRREDDAEESVSETNNHERSTPRSHAKPSLIDEPVTWITGGGTTSSRRITGS-R 299
QY 286 AALPPTPOTRRRRRRKRTIGRERKKARVLPVVVGAFLCWTPEFVVHITQALCPACSV 345
Db 300 AAATTTVYGFIERORRISLS-KERRAARFLGVINGVAVCMWLPFLVYIVPCDCCP 358
QY 346 PPRVLSAVTWLVGYNSALNPVITYVENAEFRNRVKALR 384
Db 359 SDRWVYFTWLVGYNSALNPVITYIFNQDFERRRRLILR 397

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RESULT 14

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077254 ID 077254 PRELIMINARY; PRT; 419 AA.
AC 077254;
DT 01-NOV-1998 (Tremblrel..08, Created)
DT 01-NOV-1998 (Tremblrel..08, Last sequence update)
DT 01-JUN-2001 (Tremblrel..17, Last annotation update)
DE G-PROTEIN COUPLED RECEPTOR.
OS Boophilus microplus (Cattle tick).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Boophilus.
OX NCBI_TaxID=6941;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=N-STRAIN; TISSUE=WHOLE LARVAE;
RA Baxter G.D., Barker S.C.;
RT "Isolation of an octopamine-like, G-protein coupled receptor cDNA from
RT the cattle tick, Boophilus microplus.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: A010743; CA09335.1;
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm.1.1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G-PROTEIN_RECP_F1_1.
DR PROSITE: PS50262; G-PROTEIN_RECP_F1_2.1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
SQ
SEQUENCE 419 AA; 47090 MW; 8DEDCAE2E50F3FA5 CRC64;

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Query Match 27.9%; Score 567; DB 5; Length 419;
Best Local Similarity 38.9%; Pred. No. 1; 6e-33;
Matches 142; Conservative 52; Mismatches 139; Indels 32; Gaps 11;

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QY 39 VGVALLIGAV-----LANSLVCSVATERALQPTNSFIVSLAADDLLALVLPFYVS 94
Db 58 VGTALSLSTFIVFVGVNVLICGVFNHRLPRTQVNFVLSLADLAVALLVPPENVAY 117
QY 95 EVVGGANLSPRLCDALMADVALCTASIFNLCAISVDREVAVAVPLRYNRQGGSRRL 154
Db 118 SIM-GRWVGFHGFELWLDVCTCTASILNLCAIALDRYVAIDPILNYAOKRFLR 176
QY 155 LIGATWTLISAANAAPVLCGLND---VRGRPAVCRL-EDRDYVYVSVCSFELPCMLLL 211
Db 177 SIFLWVIALISVPLPLIGMDWPEQFDETTPCRLTQETGVLTLSASGSFFIPLINSIV 236
QY 212 YMAFRLQRMWEVARAKLHGRAPRRSGPPSPPTPAPPAPELPPDPC-----GDCAPPA 266

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Db 237 YLKIF-----LATRRRLRERRA--NAAKVSSATRCATVEHVALLOERHSSSEET 287
QY 267 PGLPPDPCGSNC--APPDAVAAAL-----PQTPOTRRRRRAKIT--GREKKAMRYLPV 318
Db 288 P--PPHRCGOTTENRPSIADTSVLEONGRPPSVKFTCWEERORISISRRRARVILGI 345
QY 319 VVGAFLLCWTFPFVHVHTQALCPACSVPPRLVSAVTWLVGYNSALNPVITYVFNAAEFRRNV 378
Db 346 VMGVFVLCWTFPFIMYVTAACDHCVOGSDRLVNFITWLVGYNSALNPVITYVFNDFRRA 405
QY 379 FRKAL 383
Db 406 FRSL 410

RESULT 15
09HB49
ID 09HB49 PRELIMINARY: PRT: 462 AA.
AC 09HB49;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE ALPHA 2C ADRENERGIC RECEPTOR.
GN ADRA2C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20390061; Pubmed=10801795;
RA Small K.M., Forbes S.L., Rahman F.F., Bridges K.M., Liggett S.B.;
RT "A four amino acid deletion polymorphism in the third intracellular
RT loop of the human alpha 2C-adrenergic receptor confers impaired
RT coupling to multiple effectors."
RL J. Biol. Chem. 275:23059-23064(2000).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF280399; AAG28076.1; -.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHOPOPSN.
DR PROSITE: PS00237; G_PROTEIN_RECPEP_F1_1; 1.
DR PROSITE: PS00262; G_PROTEIN_RECPEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
FT VARIANT 239 L->R.
FT VARIANT 329 E->Q.
FT VARIANT 401 S->I.
FT VARIANT 446 R->P.
SQ SEQUENCE 462 AA; 49522 MW; EIEF9CA21ET7F6EDA CRC64;

Query Match 27.9%; Score 566; DB 4; Length 462;
Best Local Similarity 34.4%; Pred. No. 2,le-32;
Matches 157; Conservative 50; Mismatches 144; Indels 106; Gaps 14;

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Db 236 VAKLTRTLSEKRAPVGPDPGASPTTENGIGAAAGAGENGHCAPPADVEPDESSAAERR 295
QY 279 -----APPDAVAAALPQTPP----- 295
Db 296 RRGALRRGRRRAGAGAGAGADGAGPQAAESSGALTSRSPGPGRLSRASSRVEF 355
QY 296 --QTRRRRAKIT-----TGERKKAMRYLPVVGAFILCMTPFVHVHTQALC-PACSV 346
Db 356 FLRRRRARRSSVCRKVAQAAREKFTVLAVMGVFVLCWTFPFVFNDFRRA 415
QY 347 PRLVSAVTWLVGYNSALNPVITYVFNAAEFRRVFRKAL 383
Db 416 GLFFKFFFWIGYCNSLNPVITYVFNODFRRSFKHIL 452

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Search completed: February 13, 2002, 17:42:14
Job time: 195 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2002, 17:36:54 ; Search time 25.16 Seconds

(without alignments)
1139.363 Million cell updates/sec

Title: US-09-550-103-1

Perfect score: 2031
1 MGNRSTADADGLACRGPAA.....YTFVNAEFNRVERKALRACC 387

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

A_Geneseq_1101:*

1: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*

2: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*

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9: /SIDS8/gcgdata/geneseq/geneseqp/AA1988.DAT:*

10: /SIDS8/gcgdata/geneseq/geneseqp/AA1989.DAT:*

11: /SIDS8/gcgdata/geneseq/geneseqp/AA1990.DAT:*

12: /SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:*

13: /SIDS8/gcgdata/geneseq/geneseqp/AA1992.DAT:*

14: /SIDS8/gcgdata/geneseq/geneseqp/AA1993.DAT:*

15: /SIDS8/gcgdata/geneseq/geneseqp/AA1994.DAT:*

16: /SIDS8/gcgdata/geneseq/geneseqp/AA1995.DAT:*

17: /SIDS8/gcgdata/geneseq/geneseqp/AA1996.DAT:*

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19: /SIDS8/gcgdata/geneseq/geneseqp/AA1998.DAT:*

20: /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*

21: /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:*

22: /SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2031	100.0	387	AA812901	Human dopamine D4
2	2026	99.9	387	AA840503	Human dopamine D4
3	2026	99.8	387	AA870734	Human D4 dopamine
4	2026	99.8	387	AA815760	Human D4 receptor
5	2011	99.0	387	AA848948	Sequence encoded b
6	2011	99.0	387	AA896213	Recombinant human
7	2008	98.9	387	AA825335	D4 dopamine recept
8	1993	98.1	387	AA875957	Human dopamine D4
9	1993	98.1	387	AA801749	Human dopamine D4
10	1985	97.7	419	AA848949	Sequence encoded b
11	1985	97.7	419	AA896214	Recombinant human

12	1961	96.6	467	AA848950	Sequence encoded b
13	1961	96.6	467	AA896215	Recombinant human
14	1548.5	76.2	315	AA848707	G-protein coupled
15	1548.5	76.2	315	AA802679	G-protein coupled
16	1471	72.4	385	AA815759	Rat D4 receptor pr
17	683	33.6	446	AA814551	D-3 dopaminergic r
18	683	33.6	446	AA815349	D-3 dopaminergic r
19	679	33.4	400	AA824246	Human D3 dopamin
20	675	33.2	400	AA824247	Mutant human D3 do
21	659.5	32.5	414	AA811800	Human retinal dopa
22	647	31.9	415	AA805359	Rat D2 dopamine re
23	647	31.9	415	AA801598	Rat D2 dopamine re
24	646	31.8	415	AA809388	Mouse dopamine D2
25	645	31.8	443	AA805541	Human pituitary do
26	645	31.8	443	AA811497	Human pituitary do
27	645	31.8	443	AA801600	Human pituitary do
28	645	31.8	443	AA809075	Human dopamine rec
29	631.5	31.1	444	AA810544	D2 dopamine recept
30	631.5	31.1	444	AA809387	Mouse dopamine D2
31	629.5	31.0	353	AA813738	Human dopamine D2
32	607	29.9	317	AA848706	G-protein coupled
33	577	28.4	317	AA802678	G-protein coupled
34	577	28.4	447	AA800969	Human alpha2b-adre
35	575.5	28.3	450	AA800990	Human alpha2b-adre
36	564	27.8	458	AA854834	Human derived adre
37	560	27.6	314	AA848705	G-protein coupled
38	560	27.6	314	AA802677	G-protein coupled
39	559.5	27.5	379	AA833185	Corn barnacle G-pr
40	548.5	27.0	487	AA814149	Human alpha 2 beta
41	548.5	27.0	487	AA811804	Human alpha-2b adr
42	537	26.4	330	AA848659	G-protein coupled
43	537	26.4	330	AA802671	G-protein coupled
44	532.5	26.2	476	AA824089	Balanus amphitrite
45	529	26.0	601	AA821931	D.melanogaster oct

ALIGNMENTS

RESULT 1	
AA812901	AA812901 standard; protein: 387 AA.
XX	XX
AC	AA812901:
XX	XX
DT	14-NOV-2000 (first entry)
XX	XX
DE	Human dopamine D4 receptor amino acid sequence.
XX	XX
KW	Dopamine D4 receptor; human; schizophrenia; depression; diagnosis;
KW	methylation.
XX	XX
OS	Homo sapiens.
XX	XX
PN	US6080549-A.
XX	XX
PD	27-JUN-2000.
XX	XX
FE	08-APR-1997; 97US-0833703.
XX	XX
PR	08-APR-1997; 97US-0833703.
XX	XX
EA	(UYNE-) UNIV NORTHEASTERN.
XX	XX
PI	Dech RC;
XX	XX
DR	WPI; 2000-474787/41.
XX	XX
PT	Diagnosing schizophrenia or depression in an individual involves
PT	comparing phospholipid methylation levels and D4 receptor levels
PT	contributing to modified phospholipid methylation levels, to normal
PT	levels
XX	XX

PS Disclosure; Fig 1; 12pp; English.

CC The present sequence represents the human dopamine D4 receptor protein
 CC sequence. Dopamine receptors are members of the G-protein coupled
 CC receptor family. It is thought that a defect in the dopamine pathways of
 CC neuronal transmission may be involved in causing schizophrenia, with
 CC particular emphasis on the role of dopamine D4 receptors. The present
 CC invention relates to a method for assisting in the diagnosis of
 CC schizophrenia or depression in an individual and involves correlating
 CC biochemical abnormality in phospholipid methylation to abnormal
 CC modification of the dopamine D4 receptor. Normal modification of the
 CC dopamine D4 receptor occurs at the methionine residue at position 331 of
 CC the human D4 receptor protein sequence. The method is used in the
 CC diagnosis of schizophrenia or depression in an individual.

XX Sequence 387 AA;

Query Match 100.0%; Score 2031; DB 21; Length 387;
 Best Local Similarity 100.0%; Pred. No. 8.3e-146;
 Matches 387; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MGNRSTADADGILAGRPAGASAGASAGLAGGAAALVGVLLIGAVLAGNSLVCVSA 60
 DB 1 mgnrstadadgllagrpagaasagaglaaggaalvgyvlllgavlaagnslycvsa 60
 OY 61 TERALQPTNSFIVSLAADLLALLVLPFYSEVGGAWLSRRLCDALMAMVALCT 120
 DB 61 teralqptnsfivslaadllallvlpfysevggawllsprldalmamvalct 120
 OY 121 ASIFNLCAISVDRFAVAVPLRLYRNQSGSRRLIGATWLLSAVAAPVLCGLNDVGR 180
 DB 121 asifnlcaisvdrfavaavplrlrynqgsrrlllgatwllsaavaapvlgclndvgr 180
 OY 181 DPVAVRLDROVYVSVSCSFLLPCPLMLLYMATFRLOREVARRAKLRARRRPSG 240
 DB 181 dpavavrlldrovvysvscsfllpcplmllymatfrlorevarraklhgrarrpsg 240
 OY 241 PGPSPTPAPRLPDGPGDCAPAPGPPPCGSCNCAAPPVAAALPQTPQTRRR 300
 DB 241 pgpsptpaprldpgdpgdcappaglpdpccgscncappdavaaalpqtppqtrrr 300
 OY 301 RRAKITGRERKAMRVLPVVGAFLLCWTPFFVHITQALCPACSVPRPLVSAVTWLYGN 360
 DB 301 rrakitgrerkamrvlpvvgafllcwtppffvhitqalcpacsvprplvsavtwlygn 360
 OY 361 SALNPVITVFNAERNFERRALRACC 387
 DB 361 salnpvityvfnaerfnvrraklracc 387

RESULT 2

AAW40503 standard; protein; 387 AA.

AAW40503;

14-JUL-1998 (first entry).

Human dopamine D4 receptor protein.

Dopamine receptor; D4 receptor; DAR; therapy; treatment; schizophrenia;

adenosyl group; methionine adenosyl transferase; MAT deficient.

Homo sapiens.

Location/Qualifiers

34..55 /label= transmembrane_helical_element

74..96 /label= transmembrane_helical_element

110..131 /label= transmembrane_helical_element

FT Region 152..174
 FT /label= transmembrane_helical_element
 FT Region 192..213
 FT /label= transmembrane_helical_element
 FT Modified-site 313
 FT /note= "adenosyl group added"
 FT Region 315..335
 FT /label= transmembrane_helical_element
 FT Region 351..371
 FT /label= transmembrane_helical_element

US5738998-A.
 14-APR-1998.

24-MAY-1995; 95US-0449651.

24-MAY-1995; 95US-0449651.

(DETH/) DETH R C.

Deth RC;

WPI; 1998-250415/22.

Method for assessing schizophrenia treatments - by measuring modified dopamine D4 receptor levels

Disclosure; Fig 2; 15pp; English.

This sequence represents the human dopamine D4 receptor which is used in a novel method for assessing the effectiveness of a therapeutic or process for treating schizophrenia. The method involves determining the amount of dopamine D4 receptor (D4R) in a tissue sample which have and have not been modified by the addition of an adenosyl group on Met313 of the receptor. D4Rs are usually modified with the enzyme methionine adenosyl transferase (MAT), which is deficient in sufferers of schizophrenia, resulting in lower levels of the modified receptor. This method is useful for determining whether or not a treatment is effective in treating schizophrenia by detecting changes in levels of (un)modified D4R, preferably with antibodies.

Sequence 387 AA;

Query Match 99.9%; Score 2028; DB 19; Length 387;
 Best Local Similarity 99.7%; Pred. No. 1.4e-145;
 Matches 386; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 MGNRSTADADGILAGRPAGASAGASAGLAGGAAALVGVLLIGAVLAGNSLVCVSA 60
 DB 1 mgnrstadadgllagrpagaasagaglaaggaalvgyvlllgavlaagnslycvsa 60
 OY 61 TERALQPTNSFIVSLAADLLALLVLPFYSEVGGAWLSRRLCDALMAMVALCT 120
 DB 61 teralqptnsfivslaadllallvlpfysevggawllsprldalmamvalct 120
 OY 121 ASIFNLCAISVDRFAVAVPLRLYRNQSGSRRLIGATWLLSAVAAPVLCGLNDVGR 180
 DB 121 asifnlcaisvdrfavaavplrlrynqgsrrlllgatwllsaavaapvlgclndvgr 180
 OY 181 DPVAVRLDROVYVSVSCSFLLPCPLMLLYMATFRLOREVARRAKLRARRRPSG 240
 DB 181 dpavavrlldrovvysvscsfllpcplmllymatfrlorevarraklhgrarrpsg 240
 OY 241 PGPSPTPAPRLPDGPGDCAPAPGPPPCGSCNCAAPPVAAALPQTPQTRRR 300
 DB 241 pgpsptpaprldpgdpgdcappaglpdpccgscncappdavaaalpqtppqtrrr 300
 OY 301 RRAKITGRERKAMRVLPVVGAFLLCWTPFFVHITQALCPACSVPRPLVSAVTWLYGN 360
 DB 301 rrakitgrerkamrvlpvvgafllcwtppffvhitqalcpacsvprplvsavtwlygn 360

QY 361 SALNPVITYVFNAEFRNFRKALRACC 387
 Db 361 salnpvityvfnaefrnfrkallracc 387

RESULT 3

AAR70734
 ID AAR70734 standard; Protein: 387 AA.

XX AAR70734;

DT 05-AUG-1995 (first entry)

DE Human D4 dopamine receptor.

KW Dopamine receptor; neurotransmitter; dopaminergic;

KM neuroleptic; drug screening.

XX Synthetic.

PN MO9501435-A.

XX 12-JAN-1995.

PF 01-JUN-1994; 94WO-US05986.

PR 01-JUL-1993; 93US-0086439.

PA (UPJO) UPJOHN CO.

PI Chlo C, Huff RM;

XX WPI: 1995-06099/08.

DR P-PSDB: AA085071.

PT New synthetic gene for dopamine receptor - used to obtain prods.

PT for use in screening assays for activators or inhibitors or

PT assaying dopaminergic drugs.

PS Disclosure: Fig 2A-2F; 36pp; English.

XX The human D4 dopamine receptor is expressed from an artificial gene,

CC and can be used to screen compounds for D4 and dopaminergic

CC activity.

XX Sequence 387 AA;

Query Match

Best Local Similarity 99.8%; Score 2026; DB 16; Length 387;

Matches 386; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGNRSTADADGLLAGRGAAGSAGSAGLAGGGAALVGVLLIGAVLAGNSLVCVSA 60

Db 1 mgnrstadadgllagrgpaagasaglagggaalvgvlllgavlagnslycvsa 60

QY 61 TERLQPTNSFIYSLAADIALLVPLFVYSEVGGAWLSPRLCDALMAMVAALCT 120

Db 61 terlqptnsfiyslaadillalvplfvysevggawllsprldalmamvmlct 120

QY 121 ASIFNLCAISVDREAVAVPLRYNRGSGRRQLLIGATWILSAVAAPVLGGLNDVGR 180

Db 121 asifnlcaisvdravavplrynrsgsrrqllllgatwllsaavaapvlcglndivgr 180

QY 181 DPVACRLIEDRYVYSSVCSFFLPCEMLLLYWATFRLQWKEVARAKLHGRRPDSG 240

Db 181 dpvacrliedryvvyssvcsfflpcemllylwatfqlqtwelklsaaavpvcglndivgr 240

QY 241 PGPEPPPPARLPODPCGPPCAPAPGLPPDPCGNCAPPAVAAALPOTPPOTRRR 300

Db 241 pgpepppparlpdpdpcgpcapapglppdpcgncapppavaaalppqtpqrrr 300

QY 301 RRAKITGRERRAMRVLPIVVGAFLLCWPFFVVIHTQALCPACSVPLVSAVTWLGYN 360

Db 301 rrakitgrerkamrvlpivvvgafllcwpffvvhltqalcpacsvplvsaavtwlgyn 360

QY 361 SALNPVITYVFNAEFRNFRKALRACC 387

Db 361 salnpvityvfnaefrnfrkallracc 387

RESULT 4

AAB15760
 ID AAB15760 standard; Protein: 387 AA.

XX AAB15760;

DT 02-FEB-2001 (first entry)

DE Human D4 receptor protein.

KW Rat; D4 dopamine receptor; cardiovascular system; retinal tissue;

KM vasoregulator.

XX Homo sapiens.

PN US6121015-A.

XX 19-SEP-2000.

PF 07-JUN-1995; 95US-0475742.

PR 16-JUN-1994; 94US-0261293.

PR 28-JAN-1993; 93US-0014013.

XX (UNIM) UNIV WASHINGTON.

XX Todd RD, O'Malley KL;

XX WPI: 2000-655527/63.

DR N-PSDB: AAA99602.

PT Screening for compounds that selectively bind to a rat D4 dopamine

PT receptor (DDR), useful for identifying dopamine (ant)agonists,

PT comprises exposing cells transfected with a nucleic acid encoding the

PT DDR to candidate compounds

XX Disclosure: Column 27-29; 29pp; English.

PS The present sequence is the human D4 dopamine receptor. The rat

CC analogue of the human D4 receptor was isolated from a rat genomic

CC library by PCR and low stringency library screening. A cDNA encoding

CC the rat D4 dopamine receptor was expressed in transfected mammalian cells

CC and shown to preferentially bind dopamine antagonists such as clozapine.

CC The cDNA is useful for screening drugs which specifically bind to the

CC receptor and have selective effects on the cardiovascular and retinal

CC tissues through interactions with the receptor. Such compounds may act as

CC vasoregulators or may have ionotropic effects. The D4 receptor protein

CC may be used for the production of polyclonal or monoclonal antibodies

CC which recognise the D4 receptor sequence but do not recognise other

CC immunocytochemical receptors. The antibodies may be used in

CC immunocytochemical studies and for identification and isolation via

CC flow sorting of D4 expressing cell types.

SO Sequence 387 AA;

Query Match

Best Local Similarity 99.8%; Score 2026; DB 21; Length 387;

Matches 386; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGNRSTADADGLLAGRGAAGSAGSAGLAGGGAALVGVLLIGAVLAGNSLVCVSA 60

Db 1 mgnrstadadgllagrgpaagasaglagggaalvgvlllgavlagnslycvsa 60

QY 61 TERLQPTNSFIYSLAADIALLVPLFVYSEVGGAWLSPRLCDALMAMVAALCT 120

```

Db      61  teralqptnsfivslaadlllallvplfvysevggawllsprlodalmandvmlct 120
QY      121  ASINLCAISVDRFVAVAVPRLRYNROGSSRROLLLIGATWLLSAVAAPVLCGLNDVGR 180
Db      121  aslnlcaisvdrfvavaavplrynrqgsrrqlllilgatlwsaavaavplcglndvgr 180
QY      181  DPAVCRLIEDRDYVYSSVCSFFELPCPLMLLLYMATFRGLQMEVARRAKLGRAPRRPSG 240
Db      181  dpaucrledrdyvvysvcsfflpcplmlllywatfrglqmevarraklgraprrpsg 240
QY      241  PGPSPTPPAPRLPDQPCGPPCAPAPAGLPDPGSGNCAPPDAAVRAALPPQTPPQTRRR 300
Db      241  pgpsptppaprlpqdpcgpcapapaglpdpdpgsncappdavaaallppqtpqtrrr 300
QY      301  RRAKITGERKAMRVLPVVGAFLLCWTFFVHVHTQALCPAGSVPPRLVSATWMLGYVN 360
Db      301  rrakitgrerkamrvlpvvgafllcwtffvhtqalcpacsvpprlvsavtclgyvn 360
QY      361  SALNPVITYVENAEFRNFRKALRACC 387
Db      361  salnpvityvfnaefrnfrkallrac 387

RESULT 5
AAR48948
ID      AAR48948 standard; Protein: 387 AA.
XX
AC      AAR48948;
XX
DT      05-SEP-1994 (first entry)
XX
DE      Sequence encoded by allele D4.2 of the human dopamine receptor.
XX
KW      Dopamine receptor; schizophrenia; manic depression;
KW      genetic disorder; neuropsychiatric disorder; drug; RFLP;
KW      restriction fragment length polymorphism.
XX
OS      Homo sapiens.
XX
PN      M09403602-A.
XX
PD      17-FEB-1994.
XX
PF      05-AUG-1993; 93WO-US07370.
XX
PR      10-AUG-1992; 92US-0928611.
XX
PA      (UYOR-) UNIV OREGON HEALTH SCI.
XX
PI      Clivell O, Vantol HH;
XX
DR      WPI: 1994-065691/08.
DR      N-PSDB: AA057655.
XX
PT      DNA encoding human D4 dopamine receptor - used to identify
PT      restriction fragment length polymorphisms associated with genetic
PT      disorders in a population, and to screen drugs for antipsychotic
PT      activity.
XX
PS      Claim 13; Page 42-43; 70pp; English.
XX
CC      Naturally occurring alleles of the human D4 dopamine receptor gene
CC      comprise from about 2 to about 8 copies of a nucleotide sequence
CC      described in AA057654 which can be used to screen for restriction
CC      fragment length polymorphisms (RFLP's). These may be associated
CC      with genetic disorders and neuropsychiatric disorders e.g.
CC      schizophrenia and manic depression. The RFLP's may also be used
CC      to predict an individual's response to psychotropic and
CC      antipsychotic drugs. This sequence is encoded by allele D4.2 of
CC      the human dopamine receptor.
XX
SQ      Sequence 387 AA;

```

```

Query Match          99.0%; Score 2011; DB 15; Length 387;
Best Local Similarity 99.2%; Pred. No. 2.7e-144;
Matches 384; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  MGNRSTADADGDLGRCFPAAGASAGASAGLAGOGAALVGVLLIGAVLAGNSLVCVSYA 60
Db      1  mgnrstadadglagrgaagasaasaglaggaagaalvgyvlllilgavlaagnsllvcsva 60
QY      61  TERALQPTNSFIYSLAADLLALLVPLFVYSEVGGAWLLSPRLCDALMANDVALCT 120
Db      61  teralqptnsfivslaadlllallvplfvysevggawllsprlodalmandvmlct 120
QY      121  ASINLCAISVDRFVAVAVPRLRYNROGSSRROLLLIGATWLLSAVAAPVLCGLNDVGR 180
Db      121  aslnlcaisvdrfvavaavplrynrqgsrrqlllilgatlwsaavaavplcglndvgr 180
QY      181  DPAVCRLIEDRDYVYSSVCSFFELPCPLMLLLYMATFRGLQMEVARRAKLGRAPRRPSG 240
Db      181  dpaucrledrdyvvysvcsfflpcplmlllywatfrglqmevarraklgraprrpsg 240
QY      241  PGPSPTPPAPRLPDQPCGPPCAPAPAGLPDPGSGNCAPPDAAVRAALPPQTPPQTRRR 300
Db      241  pgpsptppaprlpqdpcgpcapapaglpdpdpgsncappdavaaallppqtpqtrrr 300
QY      301  RRAKITGERKAMRVLPVVGAFLLCWTFFVHVHTQALCPAGSVPPRLVSATWMLGYVN 360
Db      301  rrakitgrerkamrvlpvvgafllcwtffvhtqalcpacsvpprlvsavtclgyvn 360
QY      361  SALNPVITYVENAEFRNFRKALRACC 387
Db      361  salnpvityvfnaefrnfrkallrac 387

RESULT 6
AAR96213
ID      AAR96213 standard; Protein: 387 AA.
XX
AC      AAR96213;
XX
DT      21-NOV-1996 (first entry)
XX
DE      Recombinant human D4 dopamine receptor D4.2.
XX
KW      Dopamine; receptor; mental disorder; neurological; psychotic episode;
KW      schizophrenia; antipsychotic; psychotropic compound; manic depression;
KW      drug screening.
XX
OS      Homo sapiens.
XX
PN      US5516683-A.
XX
PD      14-MAY-1996.
XX
PF      07-DEC-1990; 90US-0626618.
XX
PR      29-APR-1993; 93US-0056051.
PR      07-DEC-1990; 90US-0626618.
PR      10-AUG-1992; 92US-0928611.
XX
PA      (UYOR-) UNIV OREGON HEALTH SCI.
XX
PI      Bunzow JR, Clivell O, Grandy DK, Van Tol HH;
XX
DR      WPI: 1996-251012/25.
DR      N-PSDB: AAT27545.
XX
PT      Recombinant expression of human D4 dopamine receptor - using a
PT      vaccinia virus vector operably linked to nucleic acid encoding the
PT      receptor in eukaryotic cells
XX
PS      Claim 2; Column 17-20; 38pp; English.

```

XX AAR96213 is a human D4 dopamine receptor, D4.2. A cDNA sequence encoding
 CC D4.2 may be inserted into a vaccinia viral vector (e.g. pZVneo)
 CC and this vector used to transform eukaryotic cells so as to express
 CC a recombinant D4 dopamine receptor (DR). Recombinant D4 DR can be
 CC used for screening potential psychotropic and antipsychotic drugs
 CC which may be useful to treat such conditions as depression and
 CC schizophrenia. Human D4 DR can also be used for the detection of
 CC dopamine or its analogues and for the production of antibodies. D4 DR
 CC is the only known clozapine-sensitive human dopamine receptor, drugs
 CC identified using D4 DR may share clozapines useful property of not
 CC inducing tardive dyskinesia and other motor side effects.

XX Sequence 387 AA;

Query Match 99.0%; Score 2011; DB 17; Length 387;
 Best Local Similarity 99.2%; Pred. No. 2,7e-144;
 Matches 384; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGNRSTADADGILAGRPAGASAGSAGLAGGGAALVGVLLIGAVLAGNSLVCSVA 60
 Db 1 mgnrstadadgllagrgaasagasaaglagggaalvgvlllgavlagnsilvcsva 60
 QY 61 TERALQPTNSFIVSLAADLLALVLPFVSEVOGAMLSPRICDALMADVALCT 120
 Db 61 teralqptnsfivslaadllalvlpfvysevggavllspricdalmandvalct 120
 QY 121 ASIFNLCAISYDRFVAAPVLRNROGSSRRQLLIGATWLLSAVAAPVLCGINDYRGR 180
 Db 121 asifnlcaisvdrfvaavplrynrngssrrqlllignatwllsaavaapvlgcindygr 180
 QY 181 DPVACRLIEDRDYVYSSVCSFLLPCPLMLLYMATFRLQWEEVARAKLHGRAPRRPSG 240
 Db 181 dpavcrliedrdyvyssvcsfllpcplmlllymatfqlgwewarraklhgraprrpsg 240
 QY 241 PGPPSPPPAPRLPQDPCGPPCAPAPGLPPDPGSGNCAPPDAAVAALPQTPPQTRRR 300
 Db 241 pgppspppaprlpqdpcgpcappapglppdpgsgncappdavaaalppqtpqtrrr 300
 QY 301 RRAKITGRERKAMRVLPVVGAFLLCWTPEFVHITQALCPACSVPPRLVSATWLGYN 360
 Db 301 rrakitgrerkamrvlpvvgafllcwtpeffvhitqalcpacsvpprlvsawtclgyn 360
 QY 361 SALNPVITYTVNAEFRRNFRKALRACC 387
 Db 361 salnpvitytvnaefrrnfrkaltacc 387

RESULT 7

AAR25335 standard; Protein: 387 AA.

XX AAR25335;

XX 06-JAN-1993 (first entry)

XX D4 dopamine receptor.

XX D2; D3; clozapine; tardive dyskinesia; schizophrenia.

XX Homo sapiens.

XX MO9210571-A.

XX 25-JUN-1992.

XX 06-DEC-1991; 91MO-US09308.

XX 07-DEC-1990; 90US-0626618.

XX (UYOR-) UNIV OREGON HEALTH SCI.

PI Civeilli O, Van Tol H;
 XX WPI: 1992-234627/28.
 DR N-PSDB; AAQ25870, AAQ25871 and AAQ25782.

XX New human dopamine D4 receptor and DNA encoding it - used to
 PT diagnose genetic diseases, expression vectors contg. the DNA are
 PT used to screen antipsychotic drugs
 XX
 BS Disclosure; Fig 2; 44pp; English.

CC The sequence given is the human dopamin D4 receptor. The receptor
 CC D4 has high homology to the other dopamine receptors D2 and D3. It
 CC has a ten fold higher affinity for clozapine, an antipsychotic drug
 CC which does not cause tardive dyskinesia or other motor side effects.
 CC This new receptor may prove useful in identifying new drugs for
 CC schizophrenia that have similar properties to clozapine. This protein
 CC has a molecular weight of 41 kD and can be produced by recombinant DNA
 CC technology. It can be used for the in vitro screening of novel
 CC antipsychotic compounds. Cells transformed by the DNA encoding this
 CC protein, to express the receptor which do not usually express it, are
 CC useful for the preparation of cell membranes for receptor binding
 CC assays and drug screening. Competitive binding assays can be used to
 CC identify agonists and antagonists. The receptor can be used for the
 CC in vivo detection of dopaminergic drugs in solution.

XX Sequence 387 AA;

Query Match 98.9%; Score 2008; DB 13; Length 387;
 Best Local Similarity 99.0%; Pred. No. 4,5e-144;
 Matches 383; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGNRSTADADGILAGRPAGASAGSAGLAGGGAALVGVLLIGAVLAGNSLVCSVA 60
 Db 1 mgnrstadadgllagrgaasagasaaglagggaalvgvlllgavlagnsilvcsva 60
 QY 61 TERALQPTNSFIVSLAADLLALVLPFVSEVOGAMLSPRICDALMADVALCT 120
 Db 61 teralqptnsfivslaadllalvlpfvysevggavllspricdalmandvalct 120
 QY 121 ASIFNLCAISYDRFVAAPVLRNROGSSRRQLLIGATWLLSAVAAPVLCGINDYRGR 180
 Db 121 asifnlcaisvdrfvaavplrynrngssrrqlllignatwllsaavaapvlgcindygr 180
 QY 181 DPVACRLIEDRDYVYSSVCSFLLPCPLMLLYMATFRLQWEEVARAKLHGRAPRRPSG 240
 Db 181 dpavcrliedrdyvyssvcsfllpcplmlllymatfqlgwewarraklhgraprrpsg 240
 QY 241 PGPPSPPPAPRLPQDPCGPPCAPAPGLPPDPGSGNCAPPDAAVAALPQTPPQTRRR 300
 Db 241 pgppspppaprlpqdpcgpcappapglppdpgsgncappdavaaalppqtpqtrrr 300
 QY 301 RRAKITGRERKAMRVLPVVGAFLLCWTPEFVHITQALCPACSVPPRLVSATWLGYN 360
 Db 301 rrakitgrerkamrvlpvvgafllcwtpeffvhitqalcpacsvpprlvsawtclgyn 360
 QY 361 SALNPVITYTVNAEFRRNFRKALRACC 387
 Db 361 salnpvitytvnaefrrnfrkaltacc 387

RESULT 8

AAR75957 standard; Protein: 387 AA.

XX AAR75957;

XX 22-DEC-1995 (first entry)

XX Human dopamine D4 receptor.

XX Restriction fragment length polymorphism; RFLP; point mutation;


```

Db      61  teralqprtsfivslaaadlllallvplfvyevvggawllsprlcalamandvmlct 120
Oy      121  ASIFNLCAISYDRVAVAAVPLRLRYNRGGSRQRLLLIGATWLLSAVAAPVLGINDVGR 180
Db      121  -sifnlcaisvdrfvavaavplrlrynrpggsrrqlllllgatwllsaavaapvlcklndvgr 179
Oy      181  DPAVCRLEDNRDYYVYSSVCSFELPCPLMLLXYMTFRGLQWVEVAR-ARKHGAPRRPS 239
Db      180  dpavcrleddyvvyssvcsfllpcplmlllywalfgltqwevarraaklhgraprrps 239
Oy      240  GPGPSPPTPPAPRLPDPCGPDCAAPAPGLPPDPCGSCNCAAPPDAVRAALPPQTPQTR 299
Db      240  gpgpssptppaprlpqdpcgpdcapapglppdpcgscncappdavrtaaalppqtpqtrr 299
Oy      300  RRRAKITGRERKAMRVLPVYVGAFLCMTPEFVHHITQALCPACSVPRILVSAVTWLGIV 359
Db      300  rrrakitgrerkamrvlpvvygaflcwtpeffvvhltqalcpacsvprilvsavtwlgyv 359
Oy      360  NSALNPVITYVFNAPFRNFRKALRACC 387
Db      360  nsalnpyityvfnafnfrvfkalracc 387

RESULT 10
AAR48949
ID  AAR48949 standard; Protein: 419 AA.
AC  AAR48949;
XX
XX
XX  05-SEP-1994 (first entry)
DT
DE  Sequence encoded by allele D4.4 of the human dopamine receptor.
XX
XX  Dopamine receptor; schizophrenia; manic depression;
KW  genetic disorder; neuropsychiatric disorder; drug; RFLP;
XX  restriction fragment length polymorphism.
OS  Homo sapiens.
XX
XX  WO9403602-A.
PN
XX  17-FEB-1994.
PD
XX
XX  05-AUG-1993; 93WO-US07370.
PF
XX  10-AUG-1992; 92US-0928611.
PR
XX  (UYOR-) UNIV OREGON HEALTH SCI.
PA
XX  Clivelli O, Vantol HH;
PI
XX  WPI; 1994-065691/08.
DR
XX  N-PSDB; AA057656.
PT
XX
XX  DNA encoding human D4 dopamine receptor - used to identify
PT  restriction fragment length polymorphisms associated with genetic
PT  disorders in a population, and to screen drugs for antipsychotic
PT  activity.
XX
XX  Claim 14; Page 46-47; 70pp; English.
XX
XX  Naturally occurring alleles of the human D4 dopamine receptor gene
CC  comprise from about 2 to about 8 copies of a nucleotide sequence
CC  described in AA057654 which can be used to screen for restriction
CC  fragment length polymorphisms (RFLP/s). These may be associated
CC  with genetic disorders and neuropsychiatric disorders e.g.
CC  schizophrenia and manic depression. The RFLP/s may also be used
CC  to predict an individual's response to psychotropic and
CC  antipsychotic drugs. This sequence is encoded by allele D4.4 of
CC  the human dopamine receptor.
XX
XX  Sequence 419 AA;

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Oy      1  MGNRSTADADGLAGRGAAGASAGSLAGCGAALVGVLLIGANVLGNSLVCVSA 60
Db      1  mgnrstadadgllagrgaagasaasagllaggaalvgvlllgavlagnsllvcvsa 60
Oy      61  TERALQPTNSFIVSLAAADLLALLVPLFVYSEVGGAWLLSPRLCDALMADVALCT 120
Db      61  teralqprtsfivslaaadlllallvplfvyevvggawllsprlcalamandvmlct 120
Oy      121  ASIFNLCAISYDRVAVAAVPLRLRYNRGGSRQRLLLIGATWLLSAVAAPVLGINDVGR 180
Db      121  asifnlcaisvdrfvavaavplrlrynrpggsrrqlllllgatwllsaavaapvlcgindvgr 180
Oy      181  DPAVCRLEDNRDYYVYSSVCSFELPCPLMLLXYMTFRGLQWVEVARAKLHGAPRRPSG 240
Db      181  dpavcrleddyvvyssvcsfllpcplmlllywalfgltqwevarraaklhgraprrpsg 240
Oy      241  GPGPSPPTPPAPR-----LPDPCGPDCAAPPAG 268
Db      241  gpgpssptppaprlpqdpcgpdcapapglprgpcgpdcapaapslpqdcgpcdappapg 300
Oy      269  LPDPCGSCNCAAPPDAVRAALPPQTPQTRRRRAKITGRERKAMRVLPVYVGAFLCMT 328
Db      301  lpdpcgscncappdavrtaaalppqtpqtrrrrakitgrerkamrvlpvvygaflcwt 360
Oy      329  PEFVHHITQALCPACSVPRILVSAVTWLGYNNSALNPVITYVFNAPFRNFRKALRACC 387
Db      361  pefvvhltqalcpacsvprilvsavtwlgyvnalsalnpyityvfnafnfrvfkalracc 419

RESULT 11
AAR96214
ID  AAR96214 standard; Protein: 419 AA.
AC  AAR96214;
XX
XX  21-NOV-1996 (first entry)
DT
DE  Recombinant human D4 dopamine receptor D4.4.
XX
XX  Dopamine; receptor; mental disorder; neurological; psychotic episode;
KW  schizophrenia; antipsychotic; psychotropic compound; manic depression;
XX  drug screening.
OS  Homo sapiens.
XX
XX  US5516683-A.
PN
XX  14-MAY-1996.
PD
XX
XX  07-DEC-1990; 90US-0626618.
PF
XX  29-APR-1993; 93US-0056051.
PR  07-DEC-1990; 90US-0626618.
PR  10-AUG-1992; 92US-0928611.
XX
XX  (UYOR-) UNIV OREGON HEALTH SCI.
PA
XX  Bunzow JR, Clivelli O, Grandy DK, Van Tol HH;
PI
XX  WPI; 1996-251012/25.
DR  N-PSDB; AAT27546.
XX
XX  Recombinant expression of human D4 dopamine receptor - using a
PT  vaccinia virus vector operably linked to nucleic acid encoding the
PT  receptor in eukaryotic cells
XX
XX  Claim 3; Column 23-24; 38pp; English.

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XX AAR96214 is a human D4 dopamine receptor, D4.4. A cDNA sequence encoding
 CC D4.4 may be inserted into a vaccinia viral vector (e.g. pZVneo)
 CC and this vector used to transform eukaryotic cells so as to express
 CC a recombinant D4 dopamine receptor (DR). Recombinant D4 DR can be
 CC used for screening potential psychotropic and antipsychotic drugs
 CC which may be useful to treat such conditions as depression and
 CC schizophrenia. Human D4 DR can also be used for the detection of
 CC dopamine or its analogues and for the production of antibodies. D4 DR
 CC is the only known clozapine-sensitive human dopamine receptor, drugs
 CC identified using D4 DR may share clozapine useful property of not
 CC inducing tardive dyskinesia and other motor side effects.

XX
 SQ Sequence 419 AA;

Query Match 97.7%; Score 1985; DB 17; Length 419;
 Best Local Similarity 91.6%; Pred. No. 2.7e-142;
 Matches 384; Conservative 0; Mismatches 3; Indels 32; Gaps 1;

DB 1 MGNRSTADADGLLAGRPAGASAGSAGLAGOGAALVGGVLLIGAVLGNLSVCSVA 60
 1 mgnrstadadgllagrpagaasagaglaaggaaalvggavlllgavlnslvcsva 60
 QY 61 TERALQPTNSFIVSLAADLLALVLPFVYSEVOGAMLSPRCDALMAMDVALCT 120
 61 teralqptnsfivslaadllalvlpfvysevgawllsprcdalmandvalct 120
 DB 61 TERALQPTNSFIVSLAADLLALVLPFVYSEVOGAMLSPRCDALMAMDVALCT 120
 61 teralqptnsfivslaadllalvlpfvysevgawllsprcdalmandvalct 120
 QY 121 ASIFNLCAISYDRVAVAAVPLRYNRGSGSRQLLIGATWLSAAVAAPVLCGLNDYRGR 180
 121 asifnlcaisydrvavaaplrynrsgsrqlllgatwlsaaavaapvlgcglndyrgr 180
 DB 121 asifnlcaisydrvavaaplrynrsgsrqlllgatwlsaaavaapvlgcglndyrgr 180
 QY 181 DPACRLEDYRDYVYSSVCSFELPCPLMLLYWATFRGLORWEYARRAKLHGRRPRPSG 240
 181 dpacrledyrdyvysvcsfelpcplmlllywatfrglorweyarraklhgrprpsg 240
 DB 181 dpacrledyrdyvysvcsfelpcplmlllywatfrglorweyarraklhgrprpsg 240
 QY 241 PGPPSPTPPAPR-----LPDPCGPDCAAPAPG 268
 241 pgppsptppaprlpqdpcgpdcaapapglprgpcgpdcaapapglpqdpcgpdcaapapg 300
 DB 241 pgppsptppaprlpqdpcgpdcaapapglprgpcgpdcaapapglpqdpcgpdcaapapg 300
 QY 269 LPPPCGSCNAPDAVRAAALPPTPOTRRRRRAKITGRERKAMRVLPVVYGAFLICWT 328
 269 lpppcgscnappdavrAAALPPTPOTRRRRRAKITGRERKAMRVLPVVYGAFLICWT 328
 DB 301 LPDPCGSCNAPDAVRAAALPPTPOTRRRRRAKITGRERKAMRVLPVVYGAFLICWT 360
 301 lppdpcgscnappdavrAAALPPTPOTRRRRRAKITGRERKAMRVLPVVYGAFLICWT 360
 QY 329 PEFVHTQALCPACSVPRPLYSATWLTGYNSALNPITYVFNAEFRRNFRKALRACC 387
 329 pefvhtqalcpacsvprplysatwltgynsalnpytyvfnaefrrnfrkalaracc 387
 DB 361 pfvhtqalcpacsvprplysatwltgynsalnpytyvfnaefrrnfrkalaracc 419

RESULT 12
 AAR48950
 ID AAR48950 standard; Protein; 467 AA.

XX AAR48950;
 AC
 DX 05-SEP-1994 (first entry)
 DT
 XX Sequence encoded by allele D4.7 of the human dopamine receptor.
 DE
 XX
 KM Dopamine receptor; schizophrenia; manic depression;
 KW genetic disorder; neuropsychiatric disorder; drug; RFLP;
 KM restriction fragment length polymorphism.
 XX
 OS Homo sapiens.
 OS
 PN W09403602-A.
 XX
 PD 17-FEB-1994.
 XX
 PF 05-AUG-1993; 93WO-US07370.
 XX
 PR 10-AUG-1992; 92US-0928611.
 XX

PA (UYOR-) UNIV OREGON HEALTH SCI.
 XX
 PI Civelli O, Vantol HH;
 XX
 DR WPI; 1994-065691/08.
 DR N-PSDB; AA057657.
 XX

PT DNA encoding human D4 dopamine receptor - used to identify
 PT restriction fragment length polymorphisms associated with genetic
 PT disorders in a population, and to screen drugs for antipsychotic
 PT activity.
 PS
 PS Claim 15; Page 50-51; 70pp; English.

CC Naturally occurring alleles of the human D4 dopamine receptor gene
 CC comprise from about 2 to about 8 copies of a nucleotide sequence
 CC described in AA057654 which can be used to screen for restriction
 CC fragment length polymorphisms (RFLP/s). These may be associated
 CC with genetic disorders and neuropsychiatric disorders e.g.
 CC schizophrenia and manic depression. The RFLP/s may also be used
 CC to predict an individual's response to psychotropic and
 CC antipsychotic drugs. This sequence is encoded by allele D4.7 of
 CC the human dopamine receptor.
 CC
 XX

SQ Sequence 467 AA;

Query Match 96.6%; Score 1961; DB 15; Length 467;
 Best Local Similarity 82.2%; Pred. No. 2e-140;
 Matches 384; Conservative 0; Mismatches 3; Indels 80; Gaps 1;

DB 1 MGNRSTADADGLLAGRPAGASAGSAGLAGOGAALVGGVLLIGAVLGNLSVCSVA 60
 1 mgnrstadadgllagrpagaasagaglaaggaaalvggavlllgavlnslvcsva 60
 QY 61 TERALQPTNSFIVSLAADLLALVLPFVYSEVOGAMLSPRCDALMAMDVALCT 120
 61 teralqptnsfivslaadllalvlpfvysevgawllsprcdalmandvalct 120
 DB 61 TERALQPTNSFIVSLAADLLALVLPFVYSEVOGAMLSPRCDALMAMDVALCT 120
 61 teralqptnsfivslaadllalvlpfvysevgawllsprcdalmandvalct 120
 QY 121 ASIFNLCAISYDRVAVAAVPLRYNRGSGSRQLLIGATWLSAAVAAPVLCGLNDYRGR 180
 121 asifnlcaisydrvavaaplrynrsgsrqlllgatwlsaaavaapvlgcglndyrgr 180
 DB 121 asifnlcaisydrvavaaplrynrsgsrqlllgatwlsaaavaapvlgcglndyrgr 180
 QY 181 DPACRLEDYRDYVYSSVCSFELPCPLMLLYWATFRGLORWEYARRAKLHGRRPRPSG 240
 181 dpacrledyrdyvysvcsfelpcplmlllywatfrglorweyarraklhgrprpsg 240
 DB 181 dpacrledyrdyvysvcsfelpcplmlllywatfrglorweyarraklhgrprpsg 240
 QY 241 PGPPSPTPPAPR-----LPDPCGPDCAAPAPG 252
 241 pgppsptppaprlpqdpcgpdcaapapglprgpcgpdcaapapglpqdpcgpdcaapapg 300
 DB 241 pgppsptppaprlpqdpcgpdcaapapglprgpcgpdcaapapglpqdpcgpdcaapapg 300
 QY 253 -----LPDPCGPDCAAPAPG 280
 253 -----LPDPCGPDCAAPAPG 280
 DB 301 LPDPCGPDCAAPAPG 360
 301 lppdpcgpdcaapapglprgpcgpdcaapapglpqdpcgpdcaapapglpqdpcgpdcaapapg 360
 QY 281 PDVRAAALPPTPOTRRRRRAKITGRERKAMRVLPVVYGAFLICWTPEFVHTQALC 340
 281 pdvraaALPPTPOTRRRRRAKITGRERKAMRVLPVVYGAFLICWTPEFVHTQALC 340
 DB 361 pdavraaALPPTPOTRRRRRAKITGRERKAMRVLPVVYGAFLICWTPEFVHTQALC 420
 361 pdavraaALPPTPOTRRRRRAKITGRERKAMRVLPVVYGAFLICWTPEFVHTQALC 420
 QY 341 PACSVPRPLYSATWLTGYNSALNPITYVFNAEFRRNFRKALRACC 387
 341 pacsvprplysatwltgynsalnpytyvfnaefrrnfrkalaracc 387
 DB 421 pacsvprplysatwltgynsalnpytyvfnaefrrnfrkalaracc 467

RESULT 13
 AAR96215
 ID AAR96215 standard; Protein; 467 AA.

XX AAR96215;
 AC
 DX 21-NOV-1996 (first entry)
 DT
 XX Recombinant human D4 dopamine receptor D4.7.
 DE

XX Dopamine; receptor; mental disorder; neurological; psychotic episode;
 KW schizophrenia; antipsychotic; psychotropic compound; manic depression;
 KW drug screening.
 OS Homo sapiens.
 XX US5516683-A.
 XX 14-MAY-1996.
 XX 07-DEC-1990; 90US-0626618.
 XX 29-APR-1993; 93US-0056051.
 XX 07-DEC-1990; 90US-0626618.
 XX 10-AUG-1992; 92US-0928611.
 PA (UNIV-) UNIV OREGON HEALTH SCI.
 PI Bunzow JR, Civeilli O, Grandy DK, Van Tol HH;
 DR WPI: 1996-251012/25.
 DR N-PSDB: AAT27547.
 XX Recombinant expression of human D4 dopamine receptor - using a
 PT vaccinia virus vector operably linked to nucleic acid encoding the
 PT receptor in eukaryotic cells
 PS Claim 4; Column 29-32; 38pp; English.
 XX AAR96215 is a human D4 dopamine receptor, D4.7. A cDNA sequence encoding
 CC D4.7 may be inserted into a vaccinia viral vector (e.g. pVNeo)
 CC and this vector used to transform eukaryotic cells so as to express
 CC a recombinant D4 dopamine receptor (DR). Recombinant D4 DR can be
 CC used for screening potential psychotropic and antipsychotic drugs
 CC which may be useful to treat such conditions as depression and
 CC schizophrenia. Human D4 DR can also be used for the detection of
 CC dopamine or its analogues and for the production of antibodies. D4 DR
 CC is the only known clozapine-sensitive human dopamine receptor. Drugs
 CC identified using D4 DR may share clozapine useful property of not
 CC inducing tardive dyskinesia and other motor side effects.
 CC
 SQ Sequence 467 AA:

Query Match 96.6%; Score 1961; DB 17; Length 467;
 Best Local Similarity 82.2%; Pred. No. 2e-140;
 Matches 384; Conservative 0; Mismatches 3; Indels 80; Gaps 1;

QY 1 MGRSRADADGLAGRPAAGASAGAGAGAAALVGVLLIGAVLAGNSLVCVSA 60
 DB 1 mqrstddadgllagrtagagasaaglaaggaalvggavlllgavlagnsllvcsva 60
 QY 61 TERALOTPTNSFIVSLAADLLALVLPFVSEVOGAMLSPRICDALMAMDAVLC 120
 DB 61 teralotptnsfivslaaadllallvlpfvysevggawllspricdalmmamdvltc 120
 QY 121 ASIFNLCAISVDRFAVAAPLRYNRGGSRRLIGATWLLSAVAAPVLCGLNDYRGR 180
 DB 121 asifnlcaisvdrfvaavaplrynrqgsrrqlllgatwllsaavaapvlcglnvdygr 180
 QY 181 DPVAVGLEDRDYVYVSSVSFPLPCLMLLYWATERGLORMVVARAKLHGAPRRPSG 240
 DB 181 dpvavgleddrvyvsvsfllpclmlllywatefgrlqtwewarraklhgraprrpsg 240
 QY 241 PGPPSPPTPAPR-----LPDPCGPDCAAPADGLPPDPCGSCAP 280
 DB 241 pgppspptpaprllpgdpcgpdccapapglprpdcgpdccapapglppdpcgpdccapapg 300
 QY 253 -----LPDPCGPDCAAPADGLPPDPCGSCAP 280
 DB 301 lpgdpcgpdccapapglprpdcgpdccapapglpgdpcgpdccapapglppdpcgscncap 360

QY 281 PDVAAALPEPQTPQTRRRRAKITGRERKAMRVLPVVGAFLCCTPFFVHTGALC 340
 DB 361 pdaviraalppqppptrrrrrrakligrckamrvlpvvgaflcctpfvhtgalc 420
 QY 341 PACSVPRPLVSATWLGYNALNPVITYVFNAEFRNVEKALRACC 387
 DB 421 pacsvprrlvsavtwlgyvnalsltpvityvfnafnrvfkalracc 467

RESULT 14
 ID AAR48707 standard; Protein; 315 AA.
 XX AAR48707;
 AC AAR48707;
 XX 05-JUN-1996 (first entry)
 DT
 XX G-protein coupled human dopamine D4 receptor protein.
 DE
 XX G-protein coupled receptor; ligand binding assay; transmembrane domain;
 KW psychotic disorder; schizophrenia; dopamine; GPCR; adenosine; thrombin;
 KW muscarinic acetylcholine; adrenergic; endothelin; bombesin; endocrine;
 KW rhodopsin; opsin; odorant; cytomagalovirus.
 XX
 OS Homo sapiens.
 XX W09405695-AI.
 XX 17-MAR-1994.
 XX 09-SEP-1993; 93MO-US08528.
 XX 10-SEP-1992; 92US-0943236.
 PA (UNIV) UNIV NEW YORK STATE.
 PI Murphy RB, Schuster DI;
 DR WPI: 1994-101120/12.
 PT Polypeptides of G-coupled receptor proteins (GPCRs) - useful for
 PT binding GPR ligands or modulating GPR binding
 PS Disclosure; Page 81; 160pp; English.
 XX Proteins AAR48685-R48758 represent a range of G-protein coupled receptor
 CC proteins selected from cAMP, adenosine, muscarinic acetylcholine,
 CC adrenergic, thrombin, endothelin, bombesin, rhodopsin, opsin,
 CC odorant, cytomagalovirus and other G-protein coupled receptors. The
 CC receptor proteins were used to design polypeptides, pref. based on the
 CC transmembrane domains, for use in G-protein coupled receptor ligand
 CC binding assays. The polypeptide fragments retain biological activity
 CC such as binding a GPR ligand or modulating GPR ligand binding to a GPR
 CC (see AAR48759-R48758, AAR50569-R50807 and AAR89189-R89195 for examples
 CC of polypeptide fragments). The polypeptide fragments can be used in
 CC compositions for treating subjects suffering from a pathology related to
 CC a GPR abnormality e.g. a psychotic disorder such as schizophrenia.
 XX
 SQ Sequence 315 AA:

Query Match 76.2%; Score 1548.5; DB 15; Length 315;
 Best Local Similarity 87.0%; Pred. No. 1.9e-109;
 Matches 308; Conservative 2; Mismatches 5; Indels 39; Gaps 4;

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 DB 1 gaalvgvlllcaavlagnsllvcsvateralqptnsfivslaaadllallvlpfvy 60
 QY 94 SEVOGAMLSPRICDALMAMDAVLCASIFNLCAISVDRFAVAAPLRYNRGGSRRL 153
 DB 61 sevggaawllspric-----dvmlctasifnlcaisvdrfvaavaplrynrqgsrrql 114

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 13, 2002, 17:37:14 ; Search time 12.69 Seconds
(without alignments)
686,271 Million cell updates/sec

Title: US-09-550-103-1

Perfect score: 2031

Sequence: 1 MGNSTADADGLAGRCPA.....YTVNAEFFRNRKALRACC 387

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
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2: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
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4: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/Backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2031	100.0	387	3 US-08-833-703-1	Sequence 1, Appl
2	2028	99.9	387	1 US-08-449-153-1	Sequence 1, Appl
3	2028	99.9	387	1 US-08-449-651-1	Sequence 1, Appl
4	2026	99.8	387	1 US-08-086-439C-3	Sequence 3, Appl
5	2026	99.8	387	1 US-08-434-877-3	Sequence 3, Appl
6	2026	99.8	387	3 US-08-475-742-4	Sequence 4, Appl
7	2017	99.3	387	1 US-07-626-618A-17	Sequence 17, Appl
8	2017	99.3	387	1 US-08-333-977-17	Sequence 17, Appl
9	2011	99.0	387	1 US-08-056-051-2	Sequence 2, Appl
10	2011	99.0	387	1 US-07-928-611-18	Sequence 18, Appl
11	2011	99.0	387	2 US-09-060-694-18	Sequence 18, Appl
12	2011	99.0	387	4 US-08-487-811A-18	Sequence 18, Appl
13	2011	99.0	387	5 PCT-US93-07370-18	Sequence 18, Appl
14	1985	97.7	419	1 US-08-056-051-4	Sequence 4, Appl
15	1985	97.7	419	1 US-07-928-611-20	Sequence 20, Appl
16	1985	97.7	419	2 US-08-487-811A-20	Sequence 20, Appl
17	1985	97.7	419	4 US-09-060-694-20	Sequence 20, Appl
18	1985	97.7	419	5 PCT-US93-07370-20	Sequence 20, Appl
19	1961	96.6	467	1 US-08-056-051-6	Sequence 6, Appl
20	1961	96.6	467	1 US-07-928-611-22	Sequence 22, Appl
21	1961	96.6	467	2 US-08-487-811A-22	Sequence 22, Appl
22	1961	96.6	467	5 US-09-060-694-22	Sequence 22, Appl
23	1961	96.6	467	5 PCT-US93-07370-22	Sequence 22, Appl
24	1548.5	76.2	315	1 US-08-118-270-28	Sequence 28, Appl
25	1548.5	76.2	315	5 PCT-US93-08528-28	Sequence 28, Appl
26	1471	72.4	385	3 US-08-475-742-2	Sequence 2, Appl
27	1016	50.0	187	1 US-07-928-611-9	Sequence 9, Appl

28	1016	50.0	187	2 US-08-487-811A-9	Sequence 9, Appl
29	1016	50.0	187	4 US-09-060-694-9	Sequence 9, Appl
30	1016	50.0	187	5 PCT-US93-07370-9	Sequence 9, Appl
31	990	48.7	219	1 US-07-928-611-11	Sequence 11, Appl
32	990	48.7	219	2 US-08-487-811A-11	Sequence 11, Appl
33	990	48.7	219	5 US-09-060-694-11	Sequence 11, Appl
34	990	48.7	219	5 PCT-US93-07370-11	Sequence 11, Appl
35	966	47.6	267	1 US-07-928-611-13	Sequence 13, Appl
36	966	47.6	267	2 US-08-487-811A-13	Sequence 13, Appl
37	966	47.6	267	5 US-09-060-694-13	Sequence 13, Appl
38	966	47.6	267	5 PCT-US93-07370-13	Sequence 13, Appl
39	744	36.6	136	1 US-07-626-618A-9	Sequence 9, Appl
40	744	36.6	136	1 US-08-333-977-9	Sequence 9, Appl
41	683	33.6	446	1 US-07-781-254A-2	Sequence 2, Appl
42	683	33.6	446	1 US-07-781-254A-3	Sequence 2, Appl
43	679	33.4	444	1 US-07-626-618A-20	Sequence 20, Appl
44	679	33.4	444	1 US-08-333-977-20	Sequence 20, Appl
45	645	31.8	443	1 US-07-626-618A-18	Sequence 18, Appl

ALIGNMENTS

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RESULT 1
US-08-833-703-1
: Sequence 1, Application US/08833703
: Patent No. 6080549
: GENERAL INFORMATION:
: APPLICANT: DETH, RICHARD
: TITLE OF INVENTION: METHODS AND MATERIALS FOR THE DIAGNOSIS AND
: TITLE OF INVENTION: TREATMENT OF SCHIZOPHRENIA AND RELATED DISORDERS
: NUMBER OF SEQUENCES: 1
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
: STREET: Ten Post Office Square
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTED for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/833,703
: FILING DATE: 08-Apr-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Helme, Ph.D., Holliday C
: REGISTRATION NUMBER: 34,346
: REFERENCE/DOCKET NUMBER: NU-431XX
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-542 2290
: TELEFAX: 617-451 0313
: TELEX:
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 387 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-08-833-703-1

Query Match 100.0%; Score 2031; DB 3; Length 387;
Best Local Similarity 100.0%; Pred. No. 5,5e-114;
Matches 387; Conservative 0; Mismatches 0; Gaps 0;
Indels 0;

1 MGNSTADADGLAGRCPAAGASAGLAGGGAALVGVLLIGAVLGNLSVCVSA 60
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Db 1 MGNSTADADGLLAGRCGPAAGASAGASAGLAGOGAAALVGVLLIGAVLAGNSLVCVSA 60
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Db 61 TERALQPTNSFIVSLAADLLALLVPLFVYSEVOGGAWLLSPRLCDALMAMVALCT 120
Qy 121 ASIFNLCAISYDRFVAFAVAVPLRYNROGSGRRQLLIGATWLLISAFAVAVPLVGLNDVGR 180
Db 121 ASIFNLCAISYDRFVAFAVAVPLRYNROGSGRRQLLIGATWLLISAFAVAVPLVGLNDVGR 180
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Qy 241 PGPPSPTPPAPRLPDPCGPDCAAPPAPGLPDPGCSNCAPPDAVRAAALPQTPPQTRRR 300
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Db 301 RRAKITGERRAMRVLPPVVGAFLLCMTPEFVHITQALCPACSVPRLSAVTWLGYVN 360
Qy 361 SALNPVIYTVFNAEFRNVRKALRACC 387
Db 361 SALNPVIYTVFNAEFRNVRKALRACC 387
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RESULT 2
US-08-449-153-1
; Sequence 1, Application US/08449153
; Patent No. 5686255
; GENERAL INFORMATION:
; APPLICANT: Deth, Richard C.
; TITLE OF INVENTION: Compositions and Methods for Diagnosing
; TITLE OF INVENTION: Schizophrenia
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millitia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,153
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Carroll, Alice O.
; REGISTRATION NUMBER: 33,542
; REFERENCE/DOCKET NUMBER: RCD95-02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 387 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-449-153-1
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Query Match 99.9%; Score 2028; DB 1; Length 387;
Best Local Similarity 99.7%; Pred. No. 8.3e-114;
Matches 386; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Db 361 SALNPVIYTVFNAEFRNVRKALRACC 387
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RESULT 3
US-08-449-651-1
; Sequence 1, Application US/08449651
; Patent No. 5738998
; GENERAL INFORMATION:
; APPLICANT: Deth, Richard C.
; TITLE OF INVENTION: Compositions and Methods for Diagnosing
; TITLE OF INVENTION: Schizophrenia
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millitia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,651
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Carroll, Alice O.
; REGISTRATION NUMBER: 33,542
; REFERENCE/DOCKET NUMBER: RCD95-02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 387 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-449-651-1
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Query Match 99.9%; Score 2028; DB 1; Length 387;
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Best Local Similarity 99.7%; Pred. No. 8.3e-114;
Matches 386; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MGNRSTADADGILLAGRPAAGASAGASAGIAGGAALVGGVLLIGAVLAGNSLVCVSA 60
QY 61 TERALOTPTNSFIYSIAAADLLALLVLPFLVYSEVGGAMLSPLRCDALMMDVALCT 120
DB 61 TERALOTPTNSFIYSIAAADLLALLVLPFLVYSEVGGAMLSPLRCDALMMDVALCT 120
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RESULT 4

US-08-086-439C-3
Sequence 3, Application US/08086439C
Patent No. 5468615
GENERAL INFORMATION:
APPLICANT: Chio, Christopher L.
TITLE OF INVENTION: A Synthetic Gene for D4 Dopamine
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Upjohn Company, Corp. Intellectual
STREET: 301 Henrietta Street
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/086,439C
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Darnley Jr., James D.
REGISTRATION NUMBER: 33,673
REFERENCE/DOCKET NUMBER: 4700
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616-385-5210
TELEFAX: 616-385-6897
TELEX: 224401
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 387 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-086-439C-3

Query Match 99.8%; Score 2026; DB 1; Length 387;
Best Local Similarity 99.7%; Pred. No. 1.1e-113;
Matches 386; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MGNRSTADADGILLAGRPAAGASAGASAGIAGGAALVGGVLLIGAVLAGNSLVCVSA 60
QY 61 TERALOTPTNSFIYSIAAADLLALLVLPFLVYSEVGGAMLSPLRCDALMMDVALCT 120
DB 61 TERALOTPTNSFIYSIAAADLLALLVLPFLVYSEVGGAMLSPLRCDALMMDVALCT 120
QY 121 ASIFNLCAISVDREFAVAAPLRYNRROGSSRRQLLIGATWLLSAVAAPVLCGLNDVGR 180
DB 121 ASIFNLCAISVDREFAVAAPLRYNRROGSSRRQLLIGATWLLSAVAAPVLCGLNDVGR 180
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DB 181 DPAVCRLEDRDYVYSSVCSFLLPCPLMLLLYATFEGLORMEVARAKLHGAPRRPSG 240
QY 241 PGPPSTPPAPRLPDPCGPDCAAPAPAGLPDPGSCNCAAPPDAVRAALPPTPPOTRRR 300
DB 241 PGPPSTPPAPRLPDPCGPDCAAPAPAGLPDPGSCNCAAPPDAVRAALPPTPPOTRRR 300
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DB 301 RRAKITGRERKAMRVLPVVVGAFLLCMTPEFVVHITQALCPACSVPRLVSAVTWLGYN 360
QY 361 SALNPVITYVFNAEFNRVFRKALRACC 387
DB 361 SALNPVITYVFNAEFNRVFRKALRACC 387
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RESULT 5

US-08-434-877-3
Sequence 3, Application US/08434877
Patent No. 5721132
GENERAL INFORMATION:
APPLICANT: Chio, Christopher L.
TITLE OF INVENTION: A Synthetic Gene for D4 Dopamine
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Upjohn Company, Corp. Intellectual
STREET: 301 Henrietta Street
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49001
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette (DS,HD)
COMPUTER: Gateway 2000, P5-90
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,877
FILING DATE: 1 July 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Darnley Jr., James D.
REGISTRATION NUMBER: 33,673
REFERENCE/DOCKET NUMBER: 4700 DVI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616-385-5210
TELEFAX: 616-385-6897
TELEX: 224401
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
 LENGTH: 387 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-434-877-3

Query Match 99.8%; Score 2026; DB 1; Length 387;
 Best Local Similarity 99.7%; Pred. No. 1.1e-113;
 Matches 386; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGNRSTADADGLLAGRPAAGASAGSAGLAGOGAALVGGVLLIGAVLGNLSVCVSA 60
 DB 1 MGNRSTADADGLLAGRPAAGASAGSAGLAGOGAALVGGVLLIGAVLGNLSVCVSA 60
 QY 61 TERALQPTNSFTVSLAAADLLALLVPLFVYSEVOGGAMLSPRICDALMAMDVALCT 120
 DB 61 TERALQPTNSFTVSLAAADLLALLVPLFVYSEVOGGAMLSPRICDALMAMDVALCT 120
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 DB 121 ASIFNLCASVDRFVAAPLRVNRGGSRRLILIGATWLLSAVAAPVLCGLNDYRGR 180
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 DB 181 DPAVCRLEDDRYVYSSVCSFELPCPLMLLLYMTFRLGLORWEVARAKLHGRAPRRPSG 240
 QY 241 PGPPSPTPPAPRLPDPCGPDCAAPAPGLPPDPCGSCAPPDAAVAALPPQTPPQTRRR 300
 DB 241 PGPPSPTPPAPRLPDPCGPDCAAPAPGLPPDPCGSCAPPDAAVAALPPQTPPQTRRR 300
 QY 301 RRAKITGRERKARVLPVYVGAFLCWTPEFVVIITQALCPACSVPPRLVSATVWLGYVN 360
 DB 301 RRAKITGRERKARVLPVYVGAFLCWTPEFVVIITQALCPACSVPPRLVSATVWLGYVN 360
 QY 361 SALNPVITYTFNNAEFNRVFRKALRACC 387
 DB 361 SALNPVITYTFNNAEFNRVFRKALRACC 387

RESULT 6
 US-08-475-742-4
 ; Sequence 4; Application US/08475742
 ; Patent No. 6121015
 ; GENERAL INFORMATION:
 ; APPLICANT: O'Malley, Karen L
 ; APPLICANT: Todd, Richard D
 ; TITLE OF INVENTION: Gene Encoding the Rat Dopamine D4 Receptor
 ; FILE REFERENCE: MU 102 CON DIV
 ; CURRENT APPLICATION NUMBER: US/08/475,742
 ; EARLIER FILING DATE: 1995-06-07
 ; EARLIER APPLICATION NUMBER: US 08/261,293
 ; EARLIER FILING DATE: 1994-06-16
 ; EARLIER APPLICATION NUMBER: US 08/014,013
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 4
 ; LENGTH: 387
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: PEPTIDE
 ; LOCATION: (1)..(387)
 ; OTHER INFORMATION: Human D4 Receptor Protein
 ; US-08-475-742-4

Query Match 99.8%; Score 2026; DB 3; Length 387;
 Best Local Similarity 99.7%; Pred. No. 1.1e-113;
 Matches 386; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGNRSTADADGLLAGRPAAGASAGSAGLAGOGAALVGGVLLIGAVLGNLSVCVSA 60
 DB 1 MGNRSTADADGLLAGRPAAGASAGSAGLAGOGAALVGGVLLIGAVLGNLSVCVSA 60
 QY 61 TERALQPTNSFTVSLAAADLLALLVPLFVYSEVOGGAMLSPRICDALMAMDVALCT 120
 DB 61 TERALQPTNSFTVSLAAADLLALLVPLFVYSEVOGGAMLSPRICDALMAMDVALCT 120
 QY 121 ASIFNLCASVDRFVAAPLRVNRGGSRRLILIGATWLLSAVAAPVLCGLNDYRGR 180
 DB 121 ASIFNLCASVDRFVAAPLRVNRGGSRRLILIGATWLLSAVAAPVLCGLNDYRGR 180
 QY 181 DPAVCRLEDDRYVYSSVCSFELPCPLMLLLYMTFRLGLORWEVARAKLHGRAPRRPSG 240
 DB 181 DPAVCRLEDDRYVYSSVCSFELPCPLMLLLYMTFRLGLORWEVARAKLHGRAPRRPSG 240
 QY 241 PGPPSPTPPAPRLPDPCGPDCAAPAPGLPPDPCGSCAPPDAAVAALPPQTPPQTRRR 300
 DB 241 PGPPSPTPPAPRLPDPCGPDCAAPAPGLPPDPCGSCAPPDAAVAALPPQTPPQTRRR 300
 QY 301 RRAKITGRERKARVLPVYVGAFLCWTPEFVVIITQALCPACSVPPRLVSATVWLGYVN 360
 DB 301 RRAKITGRERKARVLPVYVGAFLCWTPEFVVIITQALCPACSVPPRLVSATVWLGYVN 360
 QY 361 SALNPVITYTFNNAEFNRVFRKALRACC 387
 DB 361 SALNPVITYTFNNAEFNRVFRKALRACC 387

RESULT 7
 US-07-626-618A-17
 ; Sequence 17; Application US/07626618A
 ; Patent No. 5422265
 ; GENERAL INFORMATION:
 ; APPLICANT: Van Tol, Hubert H.M.
 ; APPLICANT: Civeili, Olivier
 ; TITLE OF INVENTION: A No. 5422265e1 Human Dopamine Receptor and Uses
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Allegretti & Wilcoff, Ltd.
 ; STREET: 10 South Wacker Drive, Suite 3000
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/626,618A
 ; FILING DATE: 7 DEC 1990
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 5422265nan, Kevin E
 ; REGISTRATION NUMBER: 35,303
 ; REFERENCE/DOCKET NUMBER: 90,1092
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-715-1000
 ; TELEFAX: 312-715-1234
 ; TELEX: 810-221-8317
 ; INFORMATION FOR SEQ ID NO: 17:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 387 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; US-07-626-618A-17

Query Match 99.3%; Score 2017; DB 1; Length 387;
Best Local Similarity 99.5%; Pred. No. 3.7e-113;
Matches 385; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGNRSTADADGILAGRPAAGASAGASAGIAGGAALVGVLLIGAVLAGNSLYCVSA 60
DB 1 MGNRSTADADGILAGRPAAGASAGASAGIAGGAALVGVLLIGAVLAGNSLYCVSA 60
QY 61 TERALOTPTNSFTVSLAADLLALVLPFVYSEVOGGAMLSPRICDLMADVLC 120
DB 61 TERALOTPTNSFTVSLAADLLALVLPFVYSEVOGGAMLSPRICDLMADVLC 120
QY 121 ASIFNLCAISVDREVAANVPLRYNRGGSRROLIGATWLSAAVAAPVLCGLNDYRGR 180
DB 121 ASIFNLCAISVDREVAANVPLRYNRGGSRROLIGATWLSAAVAAPVLCGLNDYRGR 180
QY 181 DPVAVCLERDQVYVSSVCSFELPCPLMLLYWATERGLORMEVARAKLHGRAPRRPSG 240
DB 181 DPVAVCLERDQVYVSSVCSFELPCPLMLLYWATERGLORMEVARAKLHGRAPRRPSG 240
QY 241 PGPPSTPPAPRLPDPCGPDCAAPAGLPDPDCGSCAPDPAVRAALPPOTPOTRRR 300
DB 241 PGPPSTPPAPRLPDPCGPDCAAPAGLPDPDCGSCAPDPAVRAALPPOTPOTRRR 300
QY 301 RRAKITGERKAMRVLPVVGAFLLCWTPEFVHHITQALCPACSVPRILVSATVTLGYVN 360
DB 301 RRAKITGERKAMRVLPVVGAFLLCWTPEFVHHITQALCPACSVPRILVSATVTLGYVN 360
QY 361 SALNPVIYTVFNAEFNRVFRKALRACC 387
DB 361 SALNPVIYTVFNAEFNRVFRKALRACC 387

RESULT 8

US-08-333-977-17
Sequence 17, Application US/08333977
Patent No. 5594108
GENERAL INFORMATION:
APPLICANT: Van Tol, Hubert H.M.
TITLE OF INVENTION: A No. 5594108el Human Dopamine Receptor and Uses
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,977
FILING DATE: 03-NOV-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/626,618
FILING DATE: 7 DEC 1990
ATTORNEY/AGENT INFORMATION:
NAME: No. 5594108nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90,1092
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1234
TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 387 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
US-08-333-977-17

Query Match 99.3%; Score 2017; DB 1; Length 387;
Best Local Similarity 99.5%; Pred. No. 3.7e-113;
Matches 385; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGNRSTADADGILAGRPAAGASAGASAGIAGGAALVGVLLIGAVLAGNSLYCVSA 60
DB 1 MGNRSTADADGILAGRPAAGASAGASAGIAGGAALVGVLLIGAVLAGNSLYCVSA 60
QY 61 TERALOTPTNSFTVSLAADLLALVLPFVYSEVOGGAMLSPRICDLMADVLC 120
DB 61 TERALOTPTNSFTVSLAADLLALVLPFVYSEVOGGAMLSPRICDLMADVLC 120
QY 121 ASIFNLCAISVDREVAANVPLRYNRGGSRROLIGATWLSAAVAAPVLCGLNDYRGR 180
DB 121 ASIFNLCAISVDREVAANVPLRYNRGGSRROLIGATWLSAAVAAPVLCGLNDYRGR 180
QY 181 DPVAVCLERDQVYVSSVCSFELPCPLMLLYWATERGLORMEVARAKLHGRAPRRPSG 240
DB 181 DPVAVCLERDQVYVSSVCSFELPCPLMLLYWATERGLORMEVARAKLHGRAPRRPSG 240
QY 241 PGPPSTPPAPRLPDPCGPDCAAPAGLPDPDCGSCAPDPAVRAALPPOTPOTRRR 300
DB 241 PGPPSTPPAPRLPDPCGPDCAAPAGLPDPDCGSCAPDPAVRAALPPOTPOTRRR 300
QY 301 RRAKITGERKAMRVLPVVGAFLLCWTPEFVHHITQALCPACSVPRILVSATVTLGYVN 360
DB 301 RRAKITGERKAMRVLPVVGAFLLCWTPEFVHHITQALCPACSVPRILVSATVTLGYVN 360
QY 361 SALNPVIYTVFNAEFNRVFRKALRACC 387
DB 361 SALNPVIYTVFNAEFNRVFRKALRACC 387

RESULT 9

US-08-056-051-2
Sequence 2, Application US/08056051
Patent No. 5516683
GENERAL INFORMATION:
APPLICANT: Grandy, David K
APPLICANT: Bunzow, James R
APPLICANT: Civeilli, Olivier
TITLE OF INVENTION: A No. 5516683el Human Dopamine Receptor and Uses
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/056,051
FILING DATE: 19930429
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5516683nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90,1092-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1234
TELEFAX: 312-715-1234

TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 387 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-056-051-2

Query Match 99.0%; Score 2011; DB 1; Length 387;
Best Local Similarity 99.2%; Pred. No. 8.5e-113;
Matches 384; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGNSTADADGGLAGRPAAGASAGASAGLAGGAAALVGGVLLIGAVLAGNSLVCVSA 60
DB 1 MGNSTADADGGLAGRPAAGASAGASAGLAGGAAALVGGVLLIGAVLAGNSLVCVSA 60
QY 61 TERALQPTNSFTVSLAAADLLALVLPLEFVSEVOGAMLSPRCLDALMAMDVALCT 120
DB 61 TERALQPTNSFTVSLAAADLLALVLPLEFVSEVOGAMLSPRCLDALMAMDVALCT 120
QY 121 ASIFNLCAISYDRVAVAAPLRYNRGSGRRQLLIGATWLLSAVAAPVLCGLNDYRGR 180
DB 121 ASIFNLCAISYDRVAVAAPLRYNRGSGRRQLLIGATWLLSAVAAPVLCGLNDYRGR 180
QY 181 DPACRLIEDRDYVYSSVCSFELPCPLMLLLYMATFPGLOMEVARRAKLHGRRAPRRSG 240
DB 181 DPACRLIEDRDYVYSSVCSFELPCPLMLLLYMATFPGLOMEVARRAKLHGRRAPRRSG 240
QY 241 PGPPSPTPPAPRLPQDCGPDCAAPAPGLPPDPGSCNCAPEDAARAALPPQTPPQTRRR 300
DB 241 PGPPSPTPPAPRLPQDCGPDCAAPAPGLPPDPGSCNCAPEDAARAALPPQTPPQTRRR 300
QY 301 RRAITGRERKAMVLYVVGAFLLCWTPEFVHIITQALCPACSVPRILVSATVWLGYVN 360
DB 301 RRAITGRERKAMVLYVVGAFLLCWTPEFVHIITQALCPACSVPRILVSATVWLGYVN 360
QY 361 SALNPVITYTFNAEFRRVFRKALRACC 387
DB 361 SALNPVITYTFNAEFRRVFRKALRACC 387

RESULT 10
US-07-928-611-18
Sequence 18, Application US/07928611
Patent No. 5569601
GENERAL INFORMATION:
APPLICANT: Van Tol, Hubert H.M.
APPLICANT: Civeili, Olivier
TITLE OF INVENTION: A No. 5569601el Human Dopamine Receptor and Uses
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/928,611
FILING DATE: 19920810
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5569601nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90,1092-B
TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 387 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-928-611-18

Query Match 99.0%; Score 2011; DB 1; Length 387;
Best Local Similarity 99.2%; Pred. No. 8.5e-113;
Matches 384; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGNSTADADGGLAGRPAAGASAGASAGLAGGAAALVGGVLLIGAVLAGNSLVCVSA 60
DB 1 MGNSTADADGGLAGRPAAGASAGASAGLAGGAAALVGGVLLIGAVLAGNSLVCVSA 60
QY 61 TERALQPTNSFTVSLAAADLLALVLPLEFVSEVOGAMLSPRCLDALMAMDVALCT 120
DB 61 TERALQPTNSFTVSLAAADLLALVLPLEFVSEVOGAMLSPRCLDALMAMDVALCT 120
QY 121 ASIFNLCAISYDRVAVAAPLRYNRGSGRRQLLIGATWLLSAVAAPVLCGLNDYRGR 180
DB 121 ASIFNLCAISYDRVAVAAPLRYNRGSGRRQLLIGATWLLSAVAAPVLCGLNDYRGR 180
QY 181 DPACRLIEDRDYVYSSVCSFELPCPLMLLLYMATFPGLOMEVARRAKLHGRRAPRRSG 240
DB 181 DPACRLIEDRDYVYSSVCSFELPCPLMLLLYMATFPGLOMEVARRAKLHGRRAPRRSG 240
QY 241 PGPPSPTPPAPRLPQDCGPDCAAPAPGLPPDPGSCNCAPEDAARAALPPQTPPQTRRR 300
DB 241 PGPPSPTPPAPRLPQDCGPDCAAPAPGLPPDPGSCNCAPEDAARAALPPQTPPQTRRR 300
QY 301 RRAITGRERKAMVLYVVGAFLLCWTPEFVHIITQALCPACSVPRILVSATVWLGYVN 360
DB 301 RRAITGRERKAMVLYVVGAFLLCWTPEFVHIITQALCPACSVPRILVSATVWLGYVN 360
QY 361 SALNPVITYTFNAEFRRVFRKALRACC 387
DB 361 SALNPVITYTFNAEFRRVFRKALRACC 387

RESULT 11
US-08-487-811A-18
Sequence 18, Application US/08487811A
Patent No. 5883226
GENERAL INFORMATION:
APPLICANT: Van Tol, Hubert H.M.
APPLICANT: Civeili, Olivier
TITLE OF INVENTION: A No. 5883226el Human Dopamine Receptor and Uses
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,811A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: No. 5883226nan, Kevin E
REGISTRATION NUMBER: 35,303

ATTORNEY/AGENT INFORMATION:

PCT-US93-07370-18

Query Match 99.08; Score 2011; DB 5; Length 387;

Best Local Similarity 99.2%; Pred. No. 8.5e-113;
Matches 384; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGNSTADADGCLLAGRPAAGASAGASAGLAGOGAALVGVLLIGAVLAGNSLVCVSA 60
DB 1 MGNSTADADGCLLAGRPAAGASAGASAGLAGOGAALVGVLLIGAVLAGNSLVCVSA 60
QY 61 TERALQPTNSFIYSLAADLLALVLPFVYSEVOGAWLSRPLCDALMADVACT 120
DB 61 TERALQPTNSFIYSLAADLLALVLPFVYSEVOGAWLSRPLCDALMADVACT 120
QY 121 ASIFNLCAISYDRVAVAVPLRYNRGGSRQLLIGATWLLSAVAAPVLCGLNDVGR 180
DB 121 ASIFNLCAISYDRVAVAVPLRYNRGGSRQLLIGATWLLSAVAAPVLCGLNDVGR 180
QY 181 DPACRLIEDRDYVYSSVCSFELPCPLMLLYMATFRGLQWEVARRAKLHGRAPRRSG 240
DB 181 DPACRLIEDRDYVYSSVCSFELPCPLMLLYMATFRGLQWEVARRAKLHGRAPRRSG 240
QY 241 PGPPSPTPPAPRLPDPCGPDCAAPAPGLPPDPGSGNCAPPDAVRAALPPQTPPQTRRR 300
DB 241 PGPPSPTPPAPRLPDPCGPDCAAPAPGLPPDPGSGNCAPPDAVRAALPPQTPPQTRRR 300
QY 301 RRAITGERRKAMRYLPPVVGAFLLCMTPEFVHITQALCPACSVPRPLVSATWLGYN 360
DB 301 RRAITGERRKAMRYLPPVVGAFLLCMTPEFVHITQALCPACSVPRPLVSATWLGYN 360
QY 361 SALNPVITYVNAEFNRVFRKALRACC 387
DB 361 SALNPVITYVNAEFNRVFRKALRACC 387

RESULT 14

US-08-056-051-4

; Sequence 4, Application US/08056051

; Patent No. 5516683

; GENERAL INFORMATION:

; APPLICANT: Grandy, David K

; APPLICANT: Bunzow, James R

; APPLICANT: Civeilli, Olivier

; APPLICANT: Van Tol, Hubert H.-M.

; TITLE OF INVENTION: A No. 5516683e1 Human Dopamine Receptor and Uses

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Allegretti & Witcoff, Ltd.

; STREET: 10 South Wacker Drive, Suite 3000

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/056,051

; FILING DATE: 19930429

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: No. 5516683nan, Kevin E

; REGISTRATION NUMBER: 35,303

; REFERENCE/DOCKET NUMBER: 90,1092-C

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312-715-1000

; TELEFAX: 312-715-1234

; TELEX: 910-221-5317

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 419 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-056-051-4

Query Match

Best Local Similarity 97.7%; Score 1985; DB 1; Length 419;

Matches 384; Conservative 0; Mismatches 3; Indels 32; Gaps 1;

QY 1 MGNSTADADGCLLAGRPAAGASAGASAGLAGOGAALVGVLLIGAVLAGNSLVCVSA 60
DB 1 MGNSTADADGCLLAGRPAAGASAGASAGLAGOGAALVGVLLIGAVLAGNSLVCVSA 60
QY 61 TERALQPTNSFIYSLAADLLALVLPFVYSEVOGAWLSRPLCDALMADVACT 120
DB 61 TERALQPTNSFIYSLAADLLALVLPFVYSEVOGAWLSRPLCDALMADVACT 120
QY 121 ASIFNLCAISYDRVAVAVPLRYNRGGSRQLLIGATWLLSAVAAPVLCGLNDVGR 180
DB 121 ASIFNLCAISYDRVAVAVPLRYNRGGSRQLLIGATWLLSAVAAPVLCGLNDVGR 180
QY 181 DPACRLIEDRDYVYSSVCSFELPCPLMLLYMATFRGLQWEVARRAKLHGRAPRRSG 240
DB 181 DPACRLIEDRDYVYSSVCSFELPCPLMLLYMATFRGLQWEVARRAKLHGRAPRRSG 240
QY 241 PGPPSPTPPAPRLPDPCGPDCAAPAPGLPPDPGSGNCAPPDAVRAALPPQTPPQTRRR 300
DB 241 PGPPSPTPPAPRLPDPCGPDCAAPAPGLPPDPGSGNCAPPDAVRAALPPQTPPQTRRR 300
QY 301 RRAITGERRKAMRYLPPVVGAFLLCMTPEFVHITQALCPACSVPRPLVSATWLGYN 360
DB 301 RRAITGERRKAMRYLPPVVGAFLLCMTPEFVHITQALCPACSVPRPLVSATWLGYN 360
QY 361 SALNPVITYVNAEFNRVFRKALRACC 387
DB 361 SALNPVITYVNAEFNRVFRKALRACC 387

RESULT 15

US-07-928-611-20

; Sequence 20, Application US/07928611

; Patent No. 5569601

; GENERAL INFORMATION:

; APPLICANT: Van Tol, Hubert H.M.

; APPLICANT: Civeilli, Olivier

; TITLE OF INVENTION: A No. 5569601e1 Human Dopamine Receptor and Uses

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Allegretti & Witcoff, Ltd.

; STREET: 10 South Wacker Drive, Suite 3000

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/928,611

; FILING DATE: 19920810

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: No. 5569601nan, Kevin E

; REGISTRATION NUMBER: 35,303

; REFERENCE/DOCKET NUMBER: 90,1092-B

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312-715-1000

; TELEFAX: 312-715-1234

; TELEX: 810-221-8317

; INFORMATION FOR SEQ ID NO: 20:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 419 amino acids

; TYPE: AMINO ACID

TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-928-611-20

Query Match 97.7%; Score 1985; DB 1; Length 419;
Best Local Similarity 91.6%; Pred. No. 3.2e-111;
Matches 384; Conservative 0; Mismatches 3; Indels 32; Gaps 1;

QY	1	MGNSTADADGLLAGRFPAGASAGASAGLAGGGAALVGVLLIGAVLAGNSLVCVSA	60
Db	1	MGNSTADADGLLAGRFPAGASAGASAGLAGGGAALVGVLLIGAVLAGNSLVCVSA	60
QY	61	TERALQPTNSFIYSLAADLLALLVPLFVYSEVGGAWLSPRLCDALMAMDVACT	120
Db	61	TERALQPTNSFIYSLAADLLALLVPLFVYSEVGGAWLSPRLCDALMAMDVACT	120
QY	121	ASIFNLCAISYDRFAVAVPLRYNRGGSSRQLLIGATWLLSAVAAPVLCGLNDVGR	180
Db	121	ASIFNLCAISYDRFAVAVPLRYNRGGSSRQLLIGATWLLSAVAAPVLCGLNDVGR	180
QY	181	DPAVCRLERDYYVYSSVCSFLLPCPLMLLYWATFGLQWEEVARAKLHGAPRRPSG	240
Db	181	DPAVCRLERDYYVYSSVCSFLLPCPLMLLYWATFGLQWEEVARAKLHGAPRRPSG	240
QY	241	PGPSPPTPPAPR-----LPDDCGPDCAAPAPG	268
Db	241	PGPSPPTPPAPRLPDDCGPDCAAPAPGLPRGCGPDCAAPAPSLPDPCGPDCAAPAPG	300
QY	269	LPPDCCGSCNCAAPPDAVRAAALFPOTPPOTRRRRRAKITGREKAMRVLPVVGAFLCMT	328
Db	301	LPPDCCGSCNCAAPPDAVRAAALFPOTPPOTRRRRRAKITGREKAMRVLPVVGAFLCMT	360
QY	329	PEFVHTITQALCPACSVPRLLVSAVTWLGYNALNPVIYTFVNAEFNRNVERKALRACC	387
Db	361	PEFVHTITQALCPACSVPRLLVSAVTWLGYNALNPVIYTFVNAEFNRNVERKALRACC	419

Search completed: February 13, 2002, 17:39:13
Job time: 119 sec

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